

WEST Search History

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DATE: Thursday, December 18, 2003

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		<i>DB=USPT,PGPB,JPAB,DWPI; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L10	(L8 and cre) and @pd > 20031218	0
<input type="checkbox"/>	L9	(L8 and L7) and @pd > 20031218	0
<input type="checkbox"/>	L8	(codon near3 mammal\$) and @pd > 20031218	0
<input type="checkbox"/>	L7	(cre recombinase) and @pd > 20031218	0
<input type="checkbox"/>	L6	(modif\$ near3 cre recombinase) and @pd > 20031218	0
<input type="checkbox"/>	L5	(L3 and cre) and @pd > 20030710	14
<input type="checkbox"/>	L4	(L3 and L2) and @pd > 20030710	7
<input type="checkbox"/>	L3	(codon near3 mammal\$) and @pd > 20030710	69
<input type="checkbox"/>	L2	(cre recombinase) and @pd > 20030710	445
<input type="checkbox"/>	L1	(modif\$ near3 cre recombinase) and @pd > 20030710	1

END OF SEARCH HISTORY



STIC SEARCH RESULTS

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or contact:

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 - Circ. Desk



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110462

SEARCH REQUEST FORM

Scientific and Technical Information Center

CRFE

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DEC 15 2003

Requester's Full Name: Celine Qian 78710
 An Unit 1636 Phone Number 306-0283 (314) Examiner # 800000 Date: 12/15/03
 Mail Box and Bldg/Room Location: 11E012/11C10 Results Format Preferred (circle) PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need. MEJ

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Modified Cre-Recombinase Gene for MammalsInventors (please provide full names): Miyagawa et al.Earliest Priority Filing Date: 9/14/00

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search for SEQ ID NO: 1

STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher _____	NA Sequence (#) <u>1</u>	STN _____
Searcher Phone # _____	AA Sequence (#) _____	Dialog _____
Searcher Location _____	Structure (#) _____	Questel Orbit _____
Date Searcher Provided: <u>12/15/03</u>	Bibliographic _____	Dr. Link _____
Date Completed: <u>12/16/03</u>	Litigation _____	Lexis Nexis _____
Searcher Prep & Review Time _____	Fulltext _____	Sequence Systems <u>01</u>
Client Prep Time _____	Patent Family _____	WWW Internet _____
On Hold Time _____	Other _____	Other (specify) _____

PT 1 500 12/15/03

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

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OM nucleic - nucleic search, using sw model
Run on: December 16, 2003, 00:09:53 ; Search time 4150 Seconds
(without alignments)
10350.628 Million cell updates/sec

Title: US-09-662-128A-1
Perfect score: 1050
Sequence: 1 atgcccagaagaagaa.....gcctgctgagagagcgac 1050

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_hgt:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_on:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vi:*

30: em_hgt_hum:*

31: em_hgt_inv:*

32: em_hgt_other:*

33: em_hgt_mus:*

34: em_hgt_pin:*

35: em_hgt_rtd:*

36: em_hgt_mam:*

37: em_hgt_vrt:*

38: em_sy:*

39: em_hgt_hum:*

40: em_hgt_mus:*

41: em_hgtg_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1050	100.0	1050	6	E63780
2	755	71.9	2346	6	AR302443
3	754.4	71.8	1032	6	AR302441
4	727.4	69.3	1080	12	AY056050
5	672.6	64.1	1725	6	AX343224
6	672.6	64.1	1725	6	AX353872
7	672.6	64.1	1800	6	AX343226
8	672.6	64.1	1800	6	AX353874
9	639.4	60.9	4960	6	AX191674
10	639.4	60.9	4960	6	AX191663
11	639.4	60.9	5365	6	AX114854
12	633.2	60.3	5894	12	AF334827
13	630	60.0	5261	6	AR222049
14	630	60.0	5261	6	AX205077
15	618.4	58.9	1553	6	AX380948
16	618.4	58.9	1553	6	AX411030
17	618.4	58.9	1553	7	WYP1CRE
18	617.4	58.8	1032	6	AX343218
19	617.4	58.8	1032	6	AX348053
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21	617.4	58.8	1032	6	AX353920
22	617.4	58.8	1074	6	AX150382
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26	617.4	58.8	1983	6	AX411753
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31	617.4	58.8	2004	6	AX191639
32	617.4	58.8	2055	6	AX191654
33	617.4	58.8	2346	6	AR302442
34	617.4	58.8	2346	6	AR302444
35	617.4	58.8	2346	6	AR302445
36	617.4	58.8	4488	6	AX191651
37	617.4	58.8	6094	6	A64973
38	617.4	58.8	6293	12	AF397196
C 39	616.8	58.7	6869	12	AF298789
C 40	616.8	58.7	6979	12	AF298780
C 41	616.8	58.7	6979	12	AF298782
C 42	616.8	58.7	7051	12	AF298785
43	616.6	58.7	4491	6	AR240211
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ALIGNMENTS

RESULT 1

E63780	E63780	1050 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	E63780	1050 bp	DNA	linear	PAT 27-AUG-2002
DEFINITION	Mammal-type Cre recombinase gene.				
ACCESSION	E63780				
VERSION	E63780.1	GI:22553618			
KEYWORDS	JP 2001086989-A/1.				
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
REFERENCE	1 (bases 1 to 1050)				
AUTHORS	Miyagawa,S. and Okabe,M.				
TITLE	Mammal-type Cre recombinase gene				
JOURNAL	Patent: JP 2001086989-A 1 03-APR-2001;				
	PRESIDENT OF OSAKA UNIVERSITY				

Pred. No. is the number of results predicted by chance to have a


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Qy 383 GCAAGGAGAACTGTGAGCGCGAGCGGCCAAGCAGCGCCCTTGCAGCGCACGG 442
Db |||||
Qy 362 GGAAGGAAAAGTGTGATCGCGCGAAAGGCGAAGCAGGCCCTCGGTTCGAGAGGACGG 421
Db |||||
Qy 443 ACTTCGACCAAGTGTGCGACCTGTATGAGAGAACAGCAGCGCTTGCAGGACATTCGCAACC 502
Db |||||
Qy 422 ATTTTCGACCAAGTGTGCGACCTGTATGAGAGAACAGCAGCGCTTGCAGGACATTAGGAC 481
Db |||||
Qy 503 TGGCCTTCTGGGATTCGCTTACACCTGTGTGCGATCGCGAGATTCGCGCGATCC 562
Db |||||
Qy 482 TGGCGTCTCTCGGAATTCATACACAGCTCTCAGGATCGCGGAATTCGCGCATTC 541
Db |||||
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Db |||||
Qy 542 GCGTGAAGCAATCAGCGCGACCGCGCGCGCTGCTGATCCACATTCGCGAGGACCA 601
Db |||||
Qy 623 AGACCTCGGTGAGCAACCGCGCGCTGTGAGAGAGCGCTTGAAGCTGTGACCAAGCTGG 682
Db |||||
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Db |||||
Qy 583 TGGAGCGCTGATCAGCTGAGCGCGGTGCGGAGCGACCCCAACCTACCTGTCTGCCC 742
Db |||||
Qy 662 TCGAACGCTGATCTCGTGTGCGGCGTCTGCGGAGCGACCCCAACCTACCTGTCTGCCC 721
Db |||||
Qy 743 GCGTGCAGAAACGCGCTGCGCGCCCGCCAGCGCCAGCGAGCTGAGCAGCGCGGCC 802
Db |||||
Qy 722 GCGTCCGAGAACCGGCTGCGCGCCCGCCAGCGCCAGCGAGCTGAGCAGCGCGGCC 781
Db |||||
Qy 803 TGGAGGCGATCTTCGAGGCGACCCACCGCGCTGATCTAGCGGCGCCAGGACGACGCGGCC 862
Db |||||
Qy 782 TGGAGGCGATCTTCGAGGCGACCCACCGCGCTGATCTAGCGGCGCCAGGACGACGCGGCC 841
Db |||||
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Db |||||
Qy 842 AACGCTACTGCGATCTGCTGCGGCGACTCGCGCGCGGTGCGCGCGCGCGCGCGCGCG 901
Db |||||
Qy 923 GCGCGCGGTGAGCATCCCGAGATCATGAGCGCGCGCGGTGCGCGCGCGCGCGCGCGCG 982
Db |||||
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Db |||||
Qy 983 TGATGAATCATCCGCAACTGAGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1042
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Qy 962 TCATGAATCATTCGCAACTTGAACGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1021
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Qy 1043 ACGCGCA 1049
Db |||||
Qy 1022 ATGCGCA 1028
Db |||||

RESULT 3
AR302441
LOCUS 1032 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 2 from patent US 6541231.
ACCESSION AR302441
VERSION AR302441.1 GI:31690708
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1032)
Unclassified.
AUTHORS Baszczyński, C.L., Iyznik, L.A., Gordon-Kamm, W.J., Guan, X., Rao, A.G.
and Tgiziani, L.A.
TITLE Method for the integration of foreign DNA into eukaryotic genomes
JOURNAL Patent: US 6541231-A 2 01-APR-2003;
FEATURES
Location/Qualifiers
source 1..1032
/organism="unknown"
BASE COUNT 228 a 326 c 301 g 177 t
ORIGIN

Query Match 71.8%; Score 754.4; DB 6; Length 1032;
Best Local Similarity 83.4%; Pred. No. 4.8e-68;
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Matches 857; Conservative 0; Mismatches 171; Indels 0; Gaps 0;
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Db |||||
Qy 83 ACGAGGTGCGCAAGAACTGTATGACATGTTTCCGAGACCGCCAGCGCTTACGCGAGACCA 142
Db |||||
Qy 62 ATGAAGTTCAGAGAACTCATGACATGTTTCCGAGACGAGCAAGCGTTACGCGAGACCA 121
Db |||||
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Db |||||
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Db |||||
Qy 422 ATTTTCGACCAAGTGTGCGACCTGTATGAGAGAACAGCAGCGCTGCGAGGACATTAAGGAA 481
Db |||||
Qy 503 TGGCTTCTCTGGGATCTGCTTACAAACCTGCTGCGCATCGCGCGAGATCGCGCGCATCC 562
Db |||||
Qy 482 TGGGCTTCTCGGATTTGCAACACGCTCTCAGGATCGCGGAAATTTGCCCGCATTC 541
Db |||||
Qy 563 GCGTGAAGGACATCAGCGCGACCGAGCGCGCGCGCTGCTGATCCACATCGCGCGCACCA 622
Db |||||
Qy 542 GCGTGAAGGACATTTAGCGCGACCGAGCGCGCGAGGATGCTTATCCACATTTGGCAGGACCA 601
Db |||||
Qy 623 AGACCTGTGAGCACCGCGCGGTGAGAGAGCGCTTGAAGCTTGGCGCTGAGCGCGCGCG 682
Db |||||
Qy 602 AGACGCTCGTTTCCACCGCAGCGCTCGAAAAGGCCCTCAGCCTCGGAGTGACCAAGCTCG 661
Db |||||
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Qy 662 TCGAACGCTGATCTCGTGTGCGGCTCGGAGACCGCGCGCGCGCGCGCGCGCGCGCGCG 721
Db |||||
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Qy 782 TGGAGGCGATTTTCGAGGCGACCCACCGCGCTGATCTAGCGGCGCCAGGACGACGCGGCC 841
Db |||||
Qy 863 AGCGCTACTGCGCTTGGAGCGGCGACAGCGCGCGCGGTGCGCGCGCGCGCGCGCGCG 922
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Db |||||
Qy 1022 ATGCTGAC 1029
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RESULT 4	AY056050	1080 bp	DNA	linear	SYN 19-NOV-2001
LOCUS	AY056050	Synthetic construct codon-optimized cre recombinase (iCre) gene, complete cds.			
DEFINITION	AY056050	Synthetic construct			
ACCESSION	AY056050.1	GI:17016299			
VERSION	AY056050.1	GI:17016299			
KEYWORDS	AY056050.1	synthetic construct			
SOURCE	AY056050.1	synthetic construct			
ORGANISM	AY056050.1	artificial sequences.			
REFERENCE	AY056050.1	1 (bases 1 to 1080)			
AUTHORS	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	Codon-Optimized Cre Recombinase Expression in the Mouse			
TITLE	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	Direct Submission			
JOURNAL	Submitted (13-SEP-2001)	Molecular Neurobiology,			
REFERENCE	Max-Planck-Institute, Jahnstr. 29, Heidelberg 69120, Germany	Location/Qualifiers			
AUTHORS	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	1..1080			
TITLE	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	/organism="synthetic construct"			
JOURNAL	Submitted (13-SEP-2001)	/mol_type="genomic DNA"			
REFERENCE	Max-Planck-Institute, Jahnstr. 29, Heidelberg 69120, Germany	/db_xref="taxon:32630"			
AUTHORS	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	/note="derived from bacteriophage P1"			
TITLE	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	1..13			
JOURNAL	Submitted (13-SEP-2001)	/note="contains Kozak sequence"			
REFERENCE	Max-Planck-Institute, Jahnstr. 29, Heidelberg 69120, Germany	14..1069			
AUTHORS	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	/gene="iCre"			
TITLE	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	/note="contains part of the large T nuclear localization signal sequence"			
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REFERENCE	Max-Planck-Institute, Jahnstr. 29, Heidelberg 69120, Germany	/transl_table=11			
AUTHORS	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	/product="codon-optimized cre recombinase"			
TITLE	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	/protein_id="AAL31698.1"			
JOURNAL	Submitted (13-SEP-2001)	/db_xref="GI:17016300"			
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AUTHORS	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	BASE COUNT			
TITLE	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	248 a 294 c 319 g 219 t			
JOURNAL	Submitted (13-SEP-2001)	ORIGIN			
REFERENCE	Max-Planck-Institute, Jahnstr. 29, Heidelberg 69120, Germany	Query Match 69.3%; Score 727.4; DB 12; Length 1080;			
AUTHORS	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	Best Local Similarity 80.8%; Pred. No. 2.6e-65;			
TITLE	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	Matches 848; Conservative 0; Mismatches 201; Indels 0; Gaps 0;			
JOURNAL	Submitted (13-SEP-2001)	2 TGCCCAAGAAGAGAGGTGACCAACCTGCTGACCGTGACACAGAACCTGCCCGCCC 61			
REFERENCE	Max-Planck-Institute, Jahnstr. 29, Heidelberg 69120, Germany	18 TGCCCAAGAAGAGAGGTGACCAACCTGCTGACCGTGACACAGAACCTGCCCGCCC 77			
AUTHORS	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	62 TGCCCGTGGACGCCACCGACGAGTGGCCGACGACCTGATGACATGTTCCCGGACC 121			
TITLE	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	78 TCCCTGTGGATGCCACCTCTGATGAAGTCAGGAAGAACCTGATGACATGTTCCAGGGACA 137			
JOURNAL	Submitted (13-SEP-2001)	122 GCCAGGCTTTCAGCGGACACACCTGGAAAGATGCTGCTGAGCGTGTGCGCAGCTGGGCGC 181			
REFERENCE	Max-Planck-Institute, Jahnstr. 29, Heidelberg 69120, Germany	138 GGCAGGCTTCTCTGAAACACACCTGGAGATGCTCTGCTGTGTGTCAGATCTTGGGCTG 197			
AUTHORS	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	182 CTTGTGCAAGTGAACACCGAAGTGGTTCCCGCCGACCGCCGAGGACGTGGCGGACT 241			
TITLE	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	198 CTTGTGCAAGTGAACACCGAAGTGGTTCCCGCTGCTGAACCTGAGGATGTGAGGGACT 257			
JOURNAL	Submitted (13-SEP-2001)	242 ACCTGCTGTACCTGACGAGCCGCGCCTGGCCGTGAAGACCATTCAGCAGACCTGGGCC 301			
REFERENCE	Max-Planck-Institute, Jahnstr. 29, Heidelberg 69120, Germany	258 ACCTCCTGTACCTGCAAGCCAGAGGCTGGCTGTGAAGACCATCAACAGACCTGGGCC 317			
AUTHORS	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	302 AGCTGAACATCTGCACCGCGCAGCGCCTGCCCGCCAGCAGACAGCAACCCGTTGA 361			
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AUTHORS	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	422 CCCTGGCCTTCGAGCGCACCGACTTCGACCAAGTGGCGGAGCTGATGAGAACAGCGACC 481			
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AUTHORS	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	902 GCGCGCCCGCGACATGCGCCGCGCGCGCTGAGCATCCCGGAGATCATGCAGCGCCGCGG 961			
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JOURNAL	Submitted (13-SEP-2001)	RESULT 5			
REFERENCE	Max-Planck-Institute, Jahnstr. 29, Heidelberg 69120, Germany	AX343224			
AUTHORS	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	LOCUS			
TITLE	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	AX343224			
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REFERENCE	Max-Planck-Institute, Jahnstr. 29, Heidelberg 69120, Germany	AX343224			
AUTHORS	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	AX343224			
TITLE	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	AX343224			
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REFERENCE	Max-Planck-Institute, Jahnstr. 29, Heidelberg 69120, Germany	GI:18491580			
AUTHORS	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	SOURCE			
TITLE	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	ORGANISM			
JOURNAL	Submitted (13-SEP-2001)	synthetic construct			
REFERENCE	Max-Planck-Institute, Jahnstr. 29, Heidelberg 69120, Germany	artificial construct			
AUTHORS	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	artificial sequences.			
TITLE	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	1			
JOURNAL	Submitted (13-SEP-2001)	Edenhofer,F.O., Wunderlich,T. and Rajewsky,K.			
REFERENCE	Max-Planck-Institute, Jahnstr. 29, Heidelberg 69120, Germany	Mutations of cryptic splice sites in cre and cre-fusion proteins to improve the expression in inducibility			
AUTHORS	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	Patent: EP 1170364-A 7 09-JAN-2002;			
TITLE	Shimshak,D.R., Kim,J., Huebner,M.R., Spergel,D.J., Buchholz,F., Stewart,F.A., Seeburg,P.H. and Sprengel,R.	ARTEMIS Pharmaceuticals GmbH (DE)			
JOURNAL	Submitted (13-SEP-2001)	PAT 01-FEB-2002			

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RESULT 9
AX191674
LOCUS AX191674 4847 bp DNA linear PAT 15-AUG-2001
DEFINITION Sequence 40 from Patent WO0149832.
ACCESSION AX191674
VERSION AX191674.1 GI:15209855
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Schwenk, F.
TITLE Transduction of recombinases for inducible gene targeting
JOURNAL Patent: WO 0149832-A 40 12-JUL-2001;
ARTEMIS Pharmaceuticals GmbH (DE)
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LOCUS AX191663 4960 bp DNA linear PAT 15-AUG-2001
DEFINITION Sequence 29 from Patent WO0149832.
ACCESSION AX191663
VERSION AX191663.1 GI:15209844
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Schwenk, F.
TITLE Transduction of recombinases for inducible gene targeting
JOURNAL Patent: WO 0149832-A 29 12-JUL-2001;
ARTEMIS Pharmaceuticals GmbH (DE)
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Query Match 60.9%; Score 639.4; DB 6; Length 4960;
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RESULT 11
AX114854LOCUS AX114854 5365 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 14 from Patent WO0129208.

ACCESSION AX114854

VERSION AX114854.1 GI:14031796

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE

AUTHORS Kuehn, R., von Melchner, H. and Altschmied, J.

TITLE Conditional gene trapping construct for the disruption of genes
JOURNAL Patent: WO 0129208-A 14 26-APR-2001;
ARTEMIS Pharmaceuticals GmbH (DE); Frankgen Biotechnologie AG (DE)
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Query Match 60.9%; Score 639.4; DB 6; Length 5365;
Best Local Similarity 75.6%; Pred. No. 1.3e-56;
Matches 793; Conservative 0; Mismatches 256; Indels 0; Gaps 0;
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Db 2272 CAGCTAAACATGCTTCACTGCTCGGTGCGCGCTGCGAGCAAGTGCAGCAATGCTGTT 2331
QY 361 AGCCTGGTGTATGCGCGCATCCGCAAGGAGACGTGACCGCGCGGAGCGCGGCGCAAGCAG 420
Db 2332 TCATCTGTTATGCGCGCGATCCGAAAGAAAAAGTTGATCCGCTGAACGTGCAAAACAG 2391
QY 421 GCCCTGGCTTCGAGCGCACCGACTTCGACAGTGGCGAGCCCTGTATGGAGAACAGCGAC 480
Db 2392 GCTCTAGCTTCGAAACGCACTGATTTGACACAGGTTCGTTCACTCATGGAATAAGCAT 2451
QY 481 CGCTGCCAGACATCCGCAACCTGGCCTTCTTGGGCATTCGCTTACAAACCCCTGCTGCGC 540
Db 2452 CGCTGCCAGGATATACGTAATCTGGCATTTCTGGGGATTCGTTATAACACCCCTGTTACGT 2511
QY 541 ATGCGCGAGATCGCGCATCCGCTGAAGAGACATCAGCCGACCGCGCGGCGCGCGCATG 600
Db 2512 ATAGCCGAAATTCGCGAGATCAGGTTAAAGATATCTACGTACTGACGGTGGAGAGATG 2571
QY 601 CTGATCCATATCGCGCACCAAGACCCCTGCTGAGCACCGCGCGCTGGAGAGAGCGCCCTG 660
Db 2572 TTAATCCATATTGGCAGAACGAAACCGTGTGTAGCACCGCAGGTGTAGAGAGGCACTT 2631
QY 661 AGCCTGGCGCTGACCAAGCTGGTGGAGCGCTGATCAGCGTGTGACGCGCTGGCGCGAGCAG 720
Db 2632 AGCCTGGGGTAACTAACTGGTGGAGCATGGATTTCCGCTCTCTGCTGTAGCTGATGAT 2691
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QY 1024 ATGTGGCGCCCTGCTGGAGGACGGCA 1049
Db 2768 ATGTGGCGCCCTGCTGCAAGATGGCA 2793

RESULT 13
LOCUS AR222049 5261 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 7 from patent US 6429001.
ACCESSION AR222049
VERSION AR222049.1 GI:23329405
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 5261)
AUTHORS Hardy,S.F.
TITLE Recombinant AAV packaging systems
JOURNAL Patent: US 6429001-A 7 06-AUG-2002;
FEATURES Location/Qualifiers
source 1..5261
/organism="unknown"
BASE COUNT 1309 a 1238 c 1329 g 1385 t
ORIGIN
Query Match 60.0%; Score 630; DB 6; Length 5261;
Best Local Similarity 75.1%; Pred. No. 1.2e-55;
Matches 786; Conservative 0; Mismatches 260; Indels 0; Gaps 0;

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Db 1201 CCAAGAAGAAGAGAGAGGTTCGAATTTACTGACCGTACACCAAAATTTGCTGCATTA 1260

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QY 184 TGTGCAAGCTGAACACCGCAAGTGTGTTCCCGCGAGCCCGAGGACGTGCGGCACTAC 243
Db 1381 TGTGCAAGTTGAATAACCGGAAATGTTTCCCGCAGAACCTGAAGATGTTCCGATTA 1440

QY 244 CTGCTGTACTGAGGCCCGCGCTGCGTGAAGACCATCCAGCAGCACTGGGCCAG 303
Db 1441 CTTCCTATCTTTCAGGCGCGCGTCTGGCAGTAAATACTATCAGCAACATTTGGGCCAG 1500

QY 304 CTGAACATGTGCAACCGCCGACGCGGCTGCCCGCCCGAGCAGCAACGCGGTGAGC 363
Db 1501 CTAAACATGTTTATGTCGGTCCGCTGCCAGCAAGTGAACAATGCTGTTTCA 1560

QY 364 CTGGTATGCGCGCATTCGCAAGGAGACGTGACCGCGGCGAGCGCGCAAGCAGGCC 423
Db 1561 CTGGTTATGCGCGGATCCGAAAGAAACGTTGATGCCGCGTGAACGTGCAAAACAGGCT 1620

QY 424 CTGGCTTCAGCGCACCGACTTCGACGAGGTGGCGACCTGATGAGAAACAGCAGCCGC 483
Db 1621 CTAGCGTTCAGACGCACTGATTTGACCCAGGTTGCTTCACTCATGGAATAATAGCGATCGC 1680

QY 484 TGCAGGACATCCGCAACCTGGCTTCTCGGGATCGCTTACACACCTGCTGCGCATC 543
Db 1681 TGCCAGGATATAGTAATCTGGCAATTTCTGGGGAATGCTTATTAACCCCTGTTACGTATA 1740

QY 544 GCCAGATCCCGCATTCGCGTGAAGGACATCAGCGGCAACCGACGCGCGCCGCGCATGCTG 603
Db 1741 GCCGAATTCGAGGATCAGGGTTAAGATATCTCAGTACTCAGCGTGGGGAATGTTA 1800

QY 604 ATCCACATCGCGCGCACCAAGACCCCTGGTGGAGCACCGCCCGCGCTGGAGAAAGGCCCTGAGC 663
Db 1801 ATCCATATTGGCAGAAACGAAACGCTGTTAGCACCGCAGTGTAGAGAAAGGCACCTTAGC 1860

QY 664 CTGGCGGTGACCAAGCTGGTGGAGCGCTGGATCAGCGTGGAGCGCGTGGCGGACGACCC 723
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QY 724 AACAACTACCTGTTCTGCCGCGTGCACAAGAACGGGCTGGCCGCCGCCCGCCAGCCACCAGC 783
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QY 784 CAGCTGAGCACCCGCGCCCTGGAGGCACTCTTCGAGGCCACCCACCGCCTGATCTACGGC 843
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RESULT 14
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LOCUS Sequence 7 from Patent WO0155361.
DEFINITION AX205077
ACCESSION AX205077
VERSION AX205077.1 GI:15394318
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 unclassified.
AUTHORS Hardy,S.F.
TITLE Recombinant aav packaging systems
JOURNAL Patent: WO 0155361-A 7 02-AUG-2001;
Chiron Corporation (US)
FEATURES Location/Qualifiers
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/note="recombinant DNA"
BASE COUNT 1309 a 1238 c 1329 g 1385 t
ORIGIN
Query Match 60.0%; Score 630; DB 6; Length 5261;
Best Local Similarity 75.1%; Pred. No. 1.2e-55;
Matches 786; Conservative 0; Mismatches 260; Indels 0; Gaps 0;

QY 4 CCCAAGAAGAGAGAGGTGAGCAACCTGTCGACCGTGACACCAAGACCTGCCCGCCCTG 63
Db 1201 CCAAGAAGAAGAGAGAGGTTCGAATTTACTGACCGTACACCAAAATTTGCTGCATTA 1260

QY 64 CCGGTGAGCCACACGAGGAGGTGCGCAAGAACCTGATGACATGTTCCGGACCGC 123
Db 1261 CCGGTGATGCAACGAGTATGAGTTTCGCAAGAACCTGATGACATGTTTCAGGGATCGC 1320

QY 124 CAGGCTTCAGCGAGCACACTGGAAGATGCTGTCGAGCGTGTGCCGACGTGGCGGCC 183
Db 1321 CAGCGTTTCTGAGCATACTGGAATAATGCTTCTGTCGGTTTCCCGGTGCTGGCGGCA 1380

QY 184 TGTGCAAGCTGAACACCGCAAGTGTGTTCCCGCGAGCCCGAGGACGTGCGGCACTAC 243
Db 1381 TGTGCAAGTTGAATAACCGGAAATGTTTCCCGCAGAACCTGAAGATGTTCCGATTA 1440

QY 244 CTGCTGTACTGAGGCCCGCGCTGCGTGAAGACCATCCAGCAGCACTGGGCCAG 303
Db 1441 CTTCCTATCTTTCAGGCGCGCGTCTGGCAGTAAATACTATCAGCAACATTTGGGCCAG 1500

QY 304 CTGAACATGTGCAACCGCCGACGCGGCTGCCCGCCCGAGCAGCAACGCGGTGAGC 363
Db 1501 CTAAACATGTTTATGTCGGTCCGCTGCCAGCAAGTGAACAATGCTGTTTCA 1560

QY 364 CTGGTATGCGCGCATTCGCAAGGAGACGTGACCGCGGCGAGCGCGCAAGCAGGCC 423
Db 1561 CTGGTTATGCGCGGATCCGAAAGAAACGTTGATGCCGCGTGAACGTGCAAAACAGGCT 1620

QY 424 CTGGCTTCAGCGCACCGACTTCGACGAGGTGGCGACCTGATGAGAAACAGCAGCCGC 483
Db 1621 CTAGCGTTCAGACGCACTGATTTGACCCAGGTTGCTTCACTCATGGAATAATAGCGATCGC 1680

QY 484 TGCAGGACATCCGCAACCTGGCTTCTCGGGATCGCTTACACACCTGCTGCGCATC 543
Db 1681 TGCCAGGATATAGTAATCTGGCAATTTCTGGGGAATGCTTATTAACCCCTGTTACGTATA 1740

QY 544 GCCAGATCCCGCATTCGCGTGAAGGACATCAGCGGCAACCGACGCGCGCCGCGCATGCTG 603
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QY	184	TGCTGCAAGCTGAACCAACCGCAAGTGGTTCCCGCCGAGCCGAGGACGTGCGGACTAC	243
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Db	1441		
QY	304	CTGAACATGCTGACCGCGCAGCGGCTGCGCCCGCCCGCCAGCAGCAGCAGCGGCTGAGC	363
Db	1501		
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QY	664	CTGGCTGACCAAGCTGGTGGAGCGTGGATCAGCTGAGCGCGTGGCGGACGCC	723
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QY	724	AACAACTACCTGTTCTGCGCGTGCAGAAACCGCGTGGCGCGCCCGCCAGCCAGC	783
Db	1921		
QY	784	CAGCTGAGCACCAGCGGCTGGAGGGCATCTTCGAGGCCACCCACCGCTGATCTACGGC	843
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QY	844	GCCAGGACGACGCGCGCAGCTGCTGCTGGAGCGGCCACAGCGCCCGCGTGGC	903
Db	2041		
QY	904	GCCGCCCGGACATGCGCCCGCGCGGTGAGCATCCCGAGATCATGCGAGCGCGCGC	963
Db	2101		
QY	964	TGGACCAAGTGAACATCGTGAATGAATCATCCGCAACCTGGACAGCAGAGACCGCGCC	1023
Db	2161		
QY	1024	ATGGTGGCTGCTGGAGGACGGCA	1049
Db	2221		
QY	1049	ATGGTGGCTGCTGGAGATGGCA	2246
Db			
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LOCUS	AX380948		linear
DEFINITION	Sequence 2 from Patent WO0210415.		PAT 18-MAR-2002
ACCESSION	AX380948		
VERSION	AX380948.1		
KEYWORDS	GI:19575790		
SOURCE	Enterobacteria phage P1		
ORGANISM	Enterobacteria phage P1		
REFERENCE	1		

AUTHORS	Li, Y., O'Donnell, C.P., Duan, H., Wu, Y.H. and Meavoy, R.									
TITLE	Methods for the controlled, automatic excision of heterologous dna from transgenic plants and dna-excising gene cassettes for use therein									
JOURNAL	Patent: WO 0210415-A 2 07-FEB-2002; The University of Connecticut (US)									
FEATURES	Location/Qualifiers									
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BASE COUNT	424 a 340 c 394 g 395 t									
ORIGIN										
Query Match	58.9%; Score 618.4; DB 6; Length 1553;									
Best Local Similarity	74.8%; Pred. No. 2.7e-54;									
Matches	775; Conservative 0; Mismatches 261; Indels 0; Gaps 0;									
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Db	477	AGTGTAAATGTCAAATTTACTGACCGGTACACCAAAATTTGCTTCGCATTACCGTGCATG	536							
QY	74	CCACGACGACGAGGTGCGCAAGAACCTGATGGACATGTTCCGCGACCGCGCAGGCTTCA	133							
Db	537	CAACGAGTGATGAGGTTCGCAAGAACCTGATGGACATGTTCCAGGATGCGCAGCGCTTT	596							
QY	134	GCGAGCACACCTGGAAGATGCTGCTGAGCGGTGTCGCGCAGCTGGCGCGCCTGTGTCAAGC	193							
Db	597	CTGAGCATACCTGGAATAATGCTTCTGTCGTTTGCCTGGTGGCGGCGCATGGTGCAGT	656							
QY	194	TGAACACCGCAAGTGGTTCCTCCGCGAGCCGAGGACGTGCGCGACTACCTGCTGTACC	253							
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QY	374	GCCGCATCCGCAAGGAGAACTGGACCCGCGCAGCGCGCCAGCAGGCCCTGCCCTTCG	433							
Db	837	GGCGGATCCGAAAAGAAAAGCTTCATCGGTGAACGTGCAAAACAGGCTCTACGGTTCG	896							
QY	434	AGCGACCGACTTCGACCCAGGTGCGCAGCTGATGGAGAACAGCGCGCTGCAGAGCA	493							
Db	897	AACGCACTGATTTGCAACGAGTTCGTTCACTCATGGAATAAGCATGCGTGCAGGATA	956							
QY	494	TCCGCAACCTGGCCTTCTTGGGATCGCCCTACAAACCTGCTGCGCATGCCGAGATCG	553							
Db	957	TACGTAATCTGGCATTTCTGGGATTTGCTTATAACACCTGTTACGTATAGCCGAAATTG	1016							
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QY	674	CCNAGCTGTGGAGCGCTGGATCAGCGTGAAGCGCGTGGCCGACGACCCCAACTACC	733							
Db	1137	CTAACTGTGCGAGCGATGATTTCCGCTCTCTGTTGTAGTATGATCCGAATACTACC	1196							
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Db	1197	TGTTTTCGCGGTGAGAAAAAATGGTGTTCGCGCGCATCTGCCACCGACGCTATCAA	1256							
QY	794	CCGCGGCCCTGGAGGGCATCTTCAGGCGCACCCACCGCCTGATCTACGGCGCCAGGACG	853							
Db	1257	CTCGCGCCTCGAAGGATTTTGAAGCAACTCATCGATTGATTTACGGCGCTAAGGATG	1316							

Qy	854	ACAGCGCCAGCGCTACCTGGCTGGAGGGCCACAGCGCCGGTGGGGCGCGCCCGCG	913
Db	1317	ACTCTGGTCAGAGATACCTGGCTGGTCTGGACACAGTGCCCGTGTGGAGCCGCGCGAG	1376
Qy	914	ACATGGCCCCGGCGCGCTGAGCATCCCCGAGATCATGAGCGCGCGGCTGGACCAACG	973
Db	1377	ATATGGCCCCGGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGGTGGCTGGACCAATG	1436
Qy	974	TGAACATCGTGATGAACCTACATCCGCAACCTGGACAGCGAGACCGGCCCATGGTGGGCC	1033
Db	1437	TAAATATTGTGTCATGAACCTATATCCGTAACCTGGATAGTGAACAGGGGCAATGGTGGGCC	1496
Qy	1034	TGCTGGAGGACGGCGA	1049
Db	1497	TGCTGGAAGATGGCGA	1512

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GenCore version 5.1.6
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues
Total number of hits satisfying chosen parameters: 5105512

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1050	100.0	1050	22	AAH41175
2	755	71.9	2346	22	Mammalian Cre reco
3	754.4	71.8	1032	22	Chimeric recombina
4	639.4	60.9	1158	24	Chimeric moCRE rec
5	639.4	60.9	4847	22	His6-NLS-Cre-MTS f
6	639.4	60.9	4960	22	pGR-crc-pA vector
7	639.4	60.9	4960	24	PCMV-I-Cre-pA vect
8	639.4	60.9	5365	22	Recombinase domain
					Retroviral vector

9	639.4	60.9	5878	24	ABT08199
10	636.4	60.6	2293	20	AAH19900
11	630	60.0	5261	22	AAH26331
12	621.8	59.2	1172	21	AAH62541
13	618.4	58.9	1553	24	ABN97179
14	618.4	58.9	1553	24	AAH35276
15	618.4	58.9	1553	24	ABK10252
16	618.4	58.9	1553	25	ABN57832
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18	617.4	58.8	1032	24	ABV76599
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21	617.4	58.8	1032	25	ABT16619
22	617.4	58.8	1074	22	AAH09257
23	617.4	58.8	1623	22	AAH09263
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25	617.4	58.8	1983	24	ABL57498
26	617.4	58.8	1983	24	ABL57499
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29	617.4	58.8	2004	22	AAH09259
30	617.4	58.8	2055	22	AAH09268
31	617.4	58.8	2346	22	AAH10216
32	617.4	58.8	2346	22	AAH10218
33	617.4	58.8	2346	22	AAH10219
34	617.4	58.8	4488	22	AAH09266
35	617.4	58.8	6094	18	AAV05703
36	617	58.8	1172	21	AAH62543
37	617	58.8	1172	21	AAH62545
38	617	58.8	1172	21	AAH62547
39	616.6	58.7	1051	22	AAH81258
40	616.6	58.7	4491	24	AAH16712
41	615.8	58.6	1125	22	AAH09267
42	615.8	58.6	4727	22	AAH09265
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ALIGNMENTS

RESULT 1
AAH41175
ID AAH41175 standard; DNA; 1050 BP.
XX AAH41175;
AC
DT 23-AUG-2001 (first entry)
XX Mammalian Cre recombinase gene.
DE
XX
XX Mammalian; Cre recombinase; organ transplantation; gene therapy;
KW animal disease model; ds.
XX
XX Mammalia.
XX
XX JP2001086989-A.
XX
PD 03-APR-2001.
XX
PF 17-SEP-1999; 99JP-0264364.
XX
PR 17-SEP-1999; 99JP-0264364.
XX
XX (OSAU) UNIV OSAKA.
PA
XX
XX WPI; 2001-360321/38.
DR P-PSDB; AAB98695.
XX
XX Mammalian type Cre recombinase gene modified so as to have a high
PT expression efficiency in a mammal by selecting a codon of high
PT frequency for use in the mammal for expressing Cre recombinase -

CC constructing stably transformed eukaryotic cells, preferably plant
CC cells. The present sequence is a chimeric recombinase DNA encoding
CC more:FLPm, Cre protein from Bacteriophage P1 and FLP from
CC Saccharomyces, both maize preferred codons.

Sequence 2346 BP; 534 A; 807 C; 599 G; 406 T; 0 other;

Query Match 71.9%; Score 755; DB 22; Length 2346;

Best Local Similarity 83.4%; Pred. No. 3.2e-102;
Matches 857; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

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QY	83	ACGAGTGGCGAAGAACCTGATGGACATGTTTCGGGACCGCAGGCGCTTCAGGAGCACA	142
Db	62	ATGAAGTCAGGAGAAACCTCATGGACATGTTCCGGACAGGAAGCGTTTCAGGAGCACA	121
QY	143	CCTGGAAGATGCTGCTGAGCGTGTCCGCAGCTGGGCGCCCTGGTGAAGCTGAACAAC	202
Db	122	CCTGGAAGATGCTGCTCCGCTCTGCGGCTCTGGGCTGCATGGTGAAGCTGAACAACA	181
QY	203	GCAAGTGTGTTCCCGCGCAGCCCGAGGACGTGGCGGCACTACCTGTGTACCTGCAAGGCC	262
Db	182	GGAACTGGTTCCTCGCTGAGCCCGAGGACGTGAGGGAATTACCTTCGTACCTGCAAGCTC	241
QY	263	GCGGCTTGCGGTGAAGACCATTCAGAGACACCTGGGCCAGCTGAAACATGCTTGACCGCC	322
Db	242	GCGGCTGGCACTGAAGACCATTCAGCAACACTTTGGACAATGAAACATGCTTCAAGCG	301
QY	323	GCAGCGGCTGCCCCCGCCCCAGCAGCAGCAACGCGCTGAGCCTGTGTGATGCGCCGATCC	382
Db	302	GCTCCGGCTCCCGGCGCCCGAGCGACTGAAAGCGCGTGAAGCCTGTGATGCGCCGATCA	361
QY	383	GCAAGGAGAACTGGACCGCCGCGAGCGCGCCAAAGCAGGCCCTTGGCTTCGAGCGCACCG	442
Db	362	GGAAAGAAACGTGATGCCGCGAAAGGCAAGCAGGCCCTCGGTTTCGAGAGGACCG	421
QY	443	ACTTCGACAGGTGCGCAGCCTGTATGGAGAAACAGCGACCGCTGCCAGGACATCCGCAACC	502
Db	422	ATTTTCGACAGGTCCGACGCTGATGGAGAACAGCGACAGGTCGCCAGGACATTAGGAACC	481
QY	503	TGGCCTTCCTGGGATCGCTTACAACACGCTGCTCGCATTCGCGAGATCGCGCCGATCC	562
Db	482	TGGCGTTCCTCGGAATTCGATACAACAGCGCTCTCAGGATCGCGAAATGCGCGCATTC	541
QY	563	CGGTGAAGGACATCAGCGCGCACCGAGCGCGCGCATGCTGATCACATTCGCGCGCACCA	622
Db	542	CGGTGAAGGACATTAGCCGCAACCGAGCGCGGAGGATGCTTATCACATTGCGAGACCA	601
QY	623	AGACCTTGTGAGCACCGCCGCGTGGAGAGGCCCTGAGCCTGGCGGCTGACCAAGCTGG	682
Db	602	AGACGCTCGTTTCCACCGCAGCGCTCGAAAAGGCCCTCAGCCTCGAGGTGACCAAGCTCG	661
QY	683	TGGAGCGTGTGATCAGCGTGAAGCGCGTGGCGCAGACCCCAAACTACTCTGTTCTGCG	742
Db	662	TCGAACGCTGTGATCTCCGTGTCCGCGCTCGCGGACGACCCAAAACACTTCTTCTGCG	721
QY	743	GCGTGGCAAGAAAGGCGTGGCCCGCCCCCAGGCGCACCGAGCTGAGACACCCGGGCC	802
Db	722	GCGTCCGCAAGAAAGGCGGTGCTGCCCCCTAGCGCCACCGACCACTCAGCAGGCGCT	781
QY	803	TGGAGGGCATCTTCAGAGCCACCCACCGCCTGATCTACGGCGCCAAAGACGACGCGGCC	862
Db	782	TGGAGGTATTTTCAGAGCCACCCACCGCCTGATCTACGGCGCGAAGATGACAGCGGTC	841
QY	863	AGCGCTACTGGCTGGAGCGGCCACAGCGCCGCGGTGGCGGCCCGCCCGACATGGGCC	922
Db	842	AACGCTACCTCGCATGTTCCGGGCACTCCGCCCCGGTTGGAGCTGTAGGACATGGGCC	901
QY	923	GCGCGCGGTGAGCATCCCGAGATCATGCAAGCGCGCGGTGGACCAACGCTGAACATCG	982

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Db 902 GGGCCGGTGTTCCTATCCCGAAATCATGTCAGCGGGTGGATGACGAAACGTGAACATTG 961
QY 983 TCATGAACATACATCCGCAACCTGCACAGCGAGACCGCGCATGCTGCCTGTGTGAGG 1042
Db 962 TCATGAACATCATTTGCAACCTTGACAGCGAGACCGCGCAATGTTGCGCTCTCTGGAAG 1021
QY 1043 ACGGCGA 1049
Db 1022 ATGGCGA 1028

RESULT 3
AAD10215
ID AAD10215 standard; DNA; 1032 BP.
XX
AC AAD10215;
XX
DT 24-SEP-2001 (first entry)
XX
Chimeric moCRE recombinase DNA.
XX
Maize; site specific recombinase; expression cassette; chimeric; moCRE;
KW Cre protein; ds.
XX
Chimeric - Zea mays.
OS Chimeric - Bacteriophage P1.
XX
Key Location/Qualifiers
FT CDS 1..1032
FT /*tag= a
FT /*product= "Chimeric moCRE protein"
XX
PN US6262341-B1.
XX
PD 17-JUL-2001.
XX
PF 17-NOV-1998; 98US-0193503.
XX
PR 18-NOV-1997; 97US-0065613.
PR 18-NOV-1997; 97US-0065627.
PR 08-SEP-1998; 98US-0099435.
XX
(PION-) PIONEER HI-BRED INT INC.
PA
XX
Baszczynski CL, Lyznik LA, Gordon-Kamm WJ, Guan X, Rao AG;
PI Tagliani LA;
XX
DR WPI; 2001-450495/48.
DR P-PSDB; AAE05410.
XX
Integrating DNA of interest into genome of eukaryotic cell, by
PT transforming plant cell with transfer cassette comprising DNA flanked
PT by target sites for site-specific recombinases and providing
PT recombinases in cell -
XX
Disclosure; Column 15-16; 30pp; English.
XX
The invention relates to compositions and methods for introducing
CC a DNA of interest into a genomic target site. The methods and
CC compositions involve the use of a combination of target sites for two
CC site specific recombinases and expression of a chimeric recombinase
CC with dual target site specificity. The compositions comprise novel
CC site-specific recombinases with specificities to multiple target sites,
CC and nucleotide sequences and expression cassettes encoding these
CC recombinases or target sites. The method of integrating the foreign DNA
CC into genome of eukaryotic cell involves transforming the cell having
CC target sites for the novel recombinase with a DNA of interest that is
CC flanked by corresponding target sites. The method is useful for
CC constructing stably transformed eukaryotic cells, preferably plant
CC cells. The present sequence is a chimeric recombinase DNA encoding
CC moCRE, Cre protein from Bacteriophage P1 with maize preferred codons.
XX
Sequence 1032 BP: 228 A; 326 C; 301G; 177 T; 0 other:

```

Query Match		71.8%;	Score 754.4;	DB 22;	Length 1032;
Best Local Similarity		83.4%;	Pred. No. 4.2e-102;		
Matches 857;		Conservative 0;	Mismatches 171;	Indels 0;	Gaps 0;
QY	23	TGAGCAACTGCTGACCGTGCACGAGACCTGCTCCGCGCTGCGCGTGGAGCGCCACCGCG	82		
Db	2	TGTCGAACCTGCTACGGTTACCAAGAACCTTCCGGCTCTTCCAGTGACGCGACGCTCCG	61		
QY	83	ACGAGGTGCGCAAGAACCTGATGACATGTTCCGCGACCGCGAGGCTTTCAGCGAGCACA	142		
Db	62	ATGAAGTCAGGAAGAACCTGATGACATGTTCCGCGACGAGCAAGCGTTACGCGAGCACA	121		
QY	143	CTGGAAGATGCTGCTAGCGTGTGCGCAGCTGGCGCGCTGTGCAAGCTGAACCAACC	202		
Db	122	CTGGAAGATGCTGCTGCTGCTGCGCTCTGCGCTGCTGCGCTGATGTTGCAAGCTGAACCA	181		
QY	203	GCAAGTGTTCCTCCGCGAGCCCGAGGACGTCGCGACTACTCTGCTACTCTGACGCGCC	262		
Db	182	GGAAGTGTTCCTCCGCTGAGCGCGAGGACGTCGCGACTACTCTGCTACTCTGACGCGCC	241		
QY	263	CGCGCTGGCGGTGAAGAACCTACAGACGACCTGGGCGCAGCTGAAATGTCACCGCC	322		
Db	242	CGCGCTGGCAGTGAAGAACCTACAGACGACCTTGGACAACTGAAATGTTACAGGC	301		
QY	323	GCAGCGGCTCCCGCGCGCGCGAGCAGCAACGCGGTGAGCTGTGATGCGCGCATCC	382		
Db	302	GCTCCGCGCTCCCGCGCGCGCGAGCTCGAACGCGCTGAGCTCTGATGCGCGCATCA	361		
QY	383	GCAAGGAGAACGTCGAGCGCGCGAGCGCGCAAGCAGGCGCTGGCGCTTCGAGCGCACG	442		
Db	362	GGAAGGAAACGTCGATGCGCGCGCAAGGCAAGCAGGCGCTCGCGTTGAGAGGACCG	421		
QY	443	ACTTCGACGAGTGGCAGCTGATGAGAACACGACCGCTGCCAGACATCGCAACC	502		
Db	422	ATTTCCGACGAGTCCGCGAGCTGATGAGAACACGACGAGCTGCCAGACATTAGGAAAC	481		
QY	503	TGGCTTCTGGGATCGCTTACAAACCTGCTGCGCATGCGCGAGATGCGCGCATCC	562		
Db	482	TGGCTTCTCGGAATTGCAACACGCTCCTCAGGATCGCGGAATTCGCCGCATTC	541		
QY	563	CGGTGAAGGACATCAGCGGACCGACCGCGCGCGCGCTGATCCATCGCGCGACCA	622		
Db	542	CGGTGAAGGACATTAGCGGACCGACCGCGCGCGAGTGTATCCATTTGGCAGGACCA	601		
QY	623	AGACCTGTGTGAGCACCGCGCGCTGGAGAGGCGCTGAGCTGGGCGTGACCAAGCTGG	682		
Db	602	AGACGCTGTTTCCACCGCAGGCGTCGAAAGGCGCTCAGCTCGGAGTGACCAAGCTCG	661		
QY	683	TGAGCGCTGGATCAGCGTGAGCGGCTGGCGCGACGACCGCCCAACACTACTGTTTGGCC	742		
Db	662	TCGAACGCTGGATCTCGGTGTCGCGCGTTCGCGGACGACCCCAACACTACTTCTTGGCC	721		
QY	743	CGGTGCGAAGACGGGTGCGCGCGCGCGCGCGCGCGCGCTGATCCATCGCGCGACCA	802		
Db	722	CGGTGCGAAGACGGGTGCGCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCTGATCC	781		
QY	803	TGAGGCGCATCTTCAGGCGCACCCACCGCGCTGATCTACGGCGCGCAAGCAGCAGCGCC	862		
Db	782	TGGAAGTATTTGAGGCGCACCCACCGCGCTGATCTACGGCGCGCAAGGATGACGCGTC	841		
QY	863	AGGCTTACTGGCTGAGCGGCGCACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	922		
Db	842	AACGCTACTCGCATGTTCCGGGCACTCCCGCGCGTTCGAGCTGTGAGGACATGCGCC	901		
QY	923	GCGCGCGCTGAGATCCCGGAGATCATGAGCGCGCGCGCGCGCGCGCGCGCGCGCG	982		
Db	902	GCGCGCGTGTTCATCCCGGAAATCATGAGCGCGCGCGCGCGCGCGCGCGCGCGCG	961		
QY	983	TGATGAATCATCCGCAACTGACAGCAGGACCGCGCGCATGCTGCGCTGCTGAGG	1042		
Db	962	TCATGAATCATTCGCAACTTGACAGCAGGCGCGCAATGTTTCGCGCTCTCTGAAG	1021		

QY	1043	ACGCGCAC 1050	
Db	1022	ATGCTGAC 1029	
RESULT 4			
ID	AAD35273 standard; DNA; 1158 BP.		
XX	AC	AAD35273;	
XX	25-JUL-2002	(first entry)	
XX	His6-NLS-Cre-MTS fusion DNA.		
XX	Site-specific DNA recombinase; DR1; membrane translocation sequence; MTS; cell-permeable recombinase; nuclear localisation signal; NLS; excretion; trafficking; blood-brain barrier; His6-NLS-Cre-MTS fusion gene; chimeric; simian virus 40; SV40; Gene; ds.		
OS	Chimeric - Rhesus macaque polyoma virus.		
OS	Chimeric - Bacteriophage P1.		
OS	Chimeric - Unidentified.		
PH	Key	Location/Qualifiers	
FT	CDS	1..1158	
FT		/*tag= a	
FT		/product= "His6-NLS-Cre-MTS fusion protein"	
FT		/transl_except= (pos: 1153..1155, aa:Pro-Glx)	
XX	WO200220737-A2.		
XX	14-MAR-2002.		
XX	07-SEP-2001; 2001WO-US28209.		
XX	07-SEP-2000; 2000US-230690P.		
XX	(UVA-) UNIV VANDERBILT.		
XX	Ruley HE, Jo D;		
XX	WPI; 2002-362248/39.		
DR	P-PSDB; AAE22205.		
XX	New isolated polypeptide comprising a cell-permeable site-specific DNA recombinase and membrane translocation sequence for stimulating site-specific DNA recombination in a cell		
PS	Claim 30; Page 42; 70pp; English.		
CC	The invention relates to a polypeptide comprising a site-specific DNA recombinase (DR1) and a membrane translocation sequence (MTS), and nucleic acids that encode such cell-permeable recombinases. The sequences of the invention are useful for stimulating site-specific DNA recombination in a cell and for determining the efficiency of protein transduction into a population of cells. The polypeptide of the invention is further useful for detecting whether site-specific DNA recombination has occurred within a cell and for identifying a compound that modulates nuclear metabolism in a cell. It is used for identifying a peptide that behaves as a membrane translocation or nuclear localisation signal (NLS) and is also useful for identifying a compound preferably an amino acid sequence that modulates the delivery of a polypeptide to a cell or the activity of a polypeptide in a cell, where the compound modulates trafficking, uptake, excretion or other activity of a specific therapeutic protein, by enhancing protein delivery across the blood-brain barrier. The present sequence is His6-NLS-Cre-MTS fusion DNA comprising cre gene from Bacteriophage P1 and Simian virus 40 NLS sequence.		
XX	Sequence 1158 BP; 287 A; 282 C; 315 G; 274 T; 0 other;		

Query Match 60.9%; Score 639.4; DB 24; Length 1158;

Best Local Similarity 75.6%; Pred. No. 2.7e-85;		Matches 793; Conservative 0; Mismatches 256; Indels 0; Gaps 0;	
QY	1	ATGCCAAGAGAGAGAGAGTGTGACCACTGCTGACCGTGACCAAGAACTGCGCCGCC	60
Db	61	ATGCCAAGAGAGAGAGAGTGTGCAATTTACTGACCGTACACCAAAATTTGCTGCA	120
QY	61	CTGCCCGTGGAGCCACACAGAGACGAGGTGCGCAAGAACCTTGATGGAATGTCGCGAC	120
Db	121	TTACCGGTGATGCAACAGAGTGTGAGGTTCGCAAGAACCTGATGACATGTTCAAGGAT	180
QY	121	CGCCAGGCTTCAGCGACACACTGGAGATGCTGCTGAGCGTGTGCGGAGCTGGGCC	180
Db	181	CGCAGGGCTTTCTGAGCATACCTGGAATGCTTCTGCTGCTTTCGGTGTGGGCG	240
QY	181	GCCTGGTCAAGCTGAACCAACCGCAAGTGGTTCGCCGCGAGCCGAGAGCTGCGCAC	240
Db	241	GCATGGTCAAGTTGAATAACCGGAATGGTTCCCGCAGAACCTGAGATGTTTCGCGAT	300
QY	241	TACCTGCTGATCTGACGCGCGGCGCTGGCGGTGAAGACATCCAGCAGCACTGGGC	300
Db	301	TATCTTCTATATCTTCAGGCGGCGGTCTGCGAGTAAAACTATCCAGCAACTTTGGGC	360
QY	301	CAGCTGAACATGCTGCACCGCGCAGCGCTGCCCCCGCCAGCAGCAGCAACGCCGTG	360
Db	361	CAGCTAAACATGCTTCATCGTGGTTCGGGCTGCCACCAAGTGACAGCAATGCTGTT	420
QY	361	AGCCTGGTGTATGCGCGCATCCGAAGGAGAACCTGTGACGCGCGAGCGGCCCAAGCAG	420
Db	421	TCACCTGGTTATGCGCGCATCCGAAGAGAAACGTTGATCGCGTGAACGTGCAACAG	480
QY	421	GGCTGGCTTCGAGCGCACCGACTTCGACAGGTGCGCAGCTGATGAGAAACAGCGAC	480
Db	481	GCTTAGCGTTTCGAACGCACTGATTTTCGACCAAGTTCGTTCACTCATGGAATAAGCAT	540
QY	481	CGCTGCAGGACATCCGCAACTCGCTTCTGCGCATCGCTACACACCTGCTGCGC	540
Db	541	CGCTGCCAGGATATACGTAATCTGCAATTCGCGGATGCTTATAACCCCTGTACGT	600
QY	541	ATCCCGAGATCGCCGCGCATCCGGTGAAGACATCAAGCCGACCGCGCGCGCATG	600
Db	601	ATAGCGGAATTCGAGATCAGGGTTAAGATATCTCACATCTACGCTGGAGATG	660
QY	601	CTGATTCACATCGCGCGCACCAACCTGTGTGACACCGCGCGTGGAGAGCCCGT	660
Db	661	TTAATCCATATGTCAGAACCAAAACGCTGTGTAGCACCGCAGGTGTAGAGAGGCACTT	720
QY	661	AGCCTGGCGTGACCAAGCTGTGGAGCTGGATCAGCGTGAGCGGTGGCGGACGAC	720
Db	721	AGCCTGGGGTAACTAACTGTCGAGCATGGATTTCCGCTCTGTGTGTAGCTGAT	780
QY	721	CCCAACAACCTACCTGTTCTGCGCGTGGCAAGAACCGCGTGGCGGCCCGCCAC	780
Db	781	CCGAATAACTACCTGTTTTCGCGGTGCAAGAAATGTTGTGTGCGCGCATCTGCCAC	840
QY	781	AGCCAGCTGACACCGCGGCTCGAGGGCATCTTCGAGGCCACCCACCGCTGATAC	840
Db	841	AGCCAGCTATCACTCGCGGCTGGAAGGATTTTGAAGCAACTCATCGATTGATTAC	900
QY	841	GGCGCCAGGACGACAGCGGCCAGCTTACCTGCGCTGGAGCGGCACAGCGCCGGTG	900
Db	901	GGCCCTAAGATGACTCTGTGAGATACCTGCGCTGGTCTGACACAGTGGCCGCTG	960
QY	901	GGCGCCGCGCGCATGGCCCGCGCGCTGAGCATCCCGGAGATCATCAGCGCGGC	960
Db	961	GGAGCGCGGAGATATGGCCCGCGCTGAGTTTCAATACCGGAGATCATCAGAGCTGT	1020
QY	961	GGCTGGACCAACGTGAACATCGTGAATCTACCTGCAACCTGGACAGGACCGGC	1020
Db	1021	GGCTGGACCAATGTAATATTTGTCATGAATATATCCGTAACCTGGATAGTGAACAGG	1080
QY	1021	GCCATGGTGGCTTCTGGAGGACGGCA	1049
Db		1081	GCAATGGTGGCGCTGCTGGAAGATGGCGA 1109
RESULT 5			
AAD09280			
ID	AAD09280	standard; DNA; 4847 BP.	
XX	AC	AAD09280;	
XX	DT	12-SEP-2001 (first entry)	
XX	DE	pgk-cre-pA vector DNA.	
XX	KW	DNA recombinase domain; protein transduction domain; PTD;	
XX	KW	gene alteration; fusion protein; Human immunodeficiency virus;	
XX	KW	HIV; pgk-cre-pA vector; ds.	
XX	OS	Unidentified.	
XX	FN	WO200149832-A2.	
XX	PD	12-JUL-2001.	
XX	PP	05-JAN-2001; 2001WO-EP00060.	
XX	PR	07-JAN-2000; 2000EP-0100351.	
XX	PR	10-NOV-2000; 2000EP-0124595.	
XX	PA	(ARTE-) ARTEMIS PHARM GMBH.	
XX	PI	Schwenk F;	
XX	DR	WPI; 2001-441873/47.	
XX	PT	Using site-specific DNA recombinase domain/protein transduction domain	
XX	PT	fusion proteins for inducing target gene alterations in organisms or	
XX	PS	cell cultures -	
XX	PS	Example; Page 67-68; 85pp; English.	
XX	CC	The present invention relates to use of fusion proteins comprising	
XX	CC	a site-specific DNA recombinase domain e.g. Cre and a protein	
XX	CC	transduction domain (PTD) e.g. the Human immunodeficiency virus	
XX	CC	(HIV) derived TAT peptide, for preparing an agent for inducing	
XX	CC	target gene alterations in a living organism or cell culture. The	
XX	CC	present invention also provides a method for inducing gene	
XX	CC	alterations in living organisms using the fusion proteins of the	
XX	CC	invention. The present sequence is a pgk-cre-pA DNA.	
XX	SQ	Sequence 4847 BP; 1139 A; 1238 C; 1283 G; 1184 T; 3 other;	
Query Match 60.9%; Score 639.4; DB 22; Length 4847;			
Best Local Similarity 75.6%; Pred. No. 2.3e-85;			
Matches 793; Conservative 0; Mismatches 256; Indels 0; Gaps 0;			
QY	1	ATGCCAAGAGAGAGAGTGTGACCACTGCTGACCGTGACCAAGAACTGCGCCGCC	60
Db	2775	ATGCCAAGAGAGAGAGTGTGCAATTTACTGACCGTACACCAAAATTTGCTGCA	2834
QY	61	CTGCCCGTGGAGCCACCGACGAGGTGCGCAAGAACCTGATGACATGTTCCGCGAC	120
Db	2835	TTACCGGTGATGCAACAGTGTGAGTTTCGCAAGAACCTGATGACATGTTCAAGGAT	2894
QY	121	CGCCAGGCTTCAGCGAGCACCTGGAAGATGCTGCTGAGCGTGTGCGGACCTGGGC	180
Db	2895	CGCCAGGCTTTCTGAGCATACCTGGAATGCTTCTGCTGCTGCTGCTGCTGCTG	2954
QY	181	GCCTGTGCAAGCTGAACACCGCAAGTGTTCCTCCCGCCGAGCCCGAGGACGTGCGGAC	240
Db	2955	GCATGTGCAAGTTGAATAACCGGAATGTTTCCCGCAGAACCTGAGATGTTCCGAT	3014
QY	241	TACCTGCTGATCTGAGGCGCGCGCTGGCGTGAAGACCATCCAGCAGCACTGGGC	300

QY 601 CTGATCCATATCGGCCCCCAACAAGACCTCGTGTGAGACCCCGCGCTGGAGAGGCGCTG 660
Db |||||
1577 TTAATCCATATTGGCAGAACGAAACCGTGTGTAGCACCGCAGGTGTAGAGAGGCACCT 1636
QY 661 AGCTGGGCTGACCAAGCTGGTGGAGCGCTGGATCAGCGTGTAGCGCGCTGGCGGAC 720
Db |||||
1637 AGCTGGGGTAACCTAAACTGGTGGAGCGATGATTTCCGTCTCTGTGTGTAGCTGATGAT 1696
QY 721 CCCAACAACTACCTGTTCTCGCGGTGCGCAAGAACGGCGTGGCGCCGCCAGCGCCACC 780
Lb |||||
1697 CCGAATAACTACCTGTTTTCGCGGTGAGAAAGTGTGTTCGCGCGCATCTGCCACC 1756
QY 781 AGCCAGCTGAGCACCCGGGCGCTGGAGGGCATTTTGAAGGCCACCCACCGCTGATCTAC 840
Db |||||
1757 AGCCAGCTATCAACTCGCGCGCTTGAAGGATTTTGAAGCAACTCATCGATTGATTTAC 1816
QY 841 GGGCCCAAGACGACGCGCGAGCTACTCGCTGGAGCGGCCACGCGCGCGCTG 900
Db |||||
1817 GGGCTAAGATGACTCTGTGAGATACCTGGCTGTGTGACACAGTGGCCCGTGC 1876
QY 901 GGGCGCCCGCGACATGGCGCGCGGTGAGCATCCCGAGATCATGCGAGCGCGC 960
Db |||||
1877 GGAGCGCGGAGATATGGCGCGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGGT 1936
QY 961 GGCTGGACCAACGTGAACATCGTGATGAATCATCGCAACTTGGACGCGAGACCGGC 1020
Db |||||
1937 GGCTGGACCAATGTAAATATTGTCACTGAACTATATCCGTAACTGGATAGTGAACAGGG 1996
QY 1021 GCCATGGTGGCGCTGCTGGAGGAGCGCA 1049
Db |||||
1997 GCAATGGTGGCGCTGCTGGAGAGTGGCA 2025

RESULT 7

ABT08148
ID ABT08148 standard; DNA; 4960 BP.

XX AC ABT08148;

XX XX 28-NOV-2002 (first entry)

XX DE Recombinase domain-containing fusion protein-related vector 4.

XX KW Fusion protein; recombinase domain; signal peptide domain; gene function;
KW nuclear import; recombinase recognition sequence; transgenic organism;
KW C31-Int recombination system; site-specific integration; gene therapy;
KW vector; ds.

XX OS Unidentified.

XX PN WO200238613-A2.

XX PD 16-MAY-2002.

XX PF 09-NOV-2001; 2001WO-EF12975.

XX PR 10-NOV-2000; 2000EP-0124629.

XX PR 17-APR-2001; 2001EP-0109543.

XX PR 13-AUG-2001; 2001US-311876P.

XX PA (ARTE-) ARTEMIS PHARM GMBH.

XX PI Kuehn R, Felder S, Schwenk F, Kueter-luks B, Faust N;

XX DR WPI; 2002-519298/55.

XX PT Novel fusion protein useful for recombining DNA molecules in eukaryotic

XX PT cells has recombinase protein which is linked to signal peptide domain

XX PT which directs nuclear import of fusion protein in eukaryotic cells -

XX PS Example 1; Page 55-56; 150pp; English.

XX XX

CC The invention comprises the amino acid and coding sequences of fusion
CC proteins that contain a recombinase domain and a signal peptide domain
CC which directs nuclear import of the fusion protein in eukaryotic cells.
CC The fusion proteins of the invention are useful for recombining the DNA
CC molecules of cells or organisms containing recombinase recognition
CC sequences for the recombinase domain of the fusion proteins. The fusion
CC proteins of the invention are useful for studying gene function at
CC various developmental stages and for the creation of transgenic
CC organisms. The C31-Int recombination system of the invention can be used
CC for the site-specific integration of foreign DNA into the genome of
CC mammalian cells (e.g. for gene therapy). The present DNA sequence
CC represents a vector that was used in the invention.

XX XX

SQ Sequence 4960 BP; 1225 A; 1213 C; 1296 G; 1226 T; 0 other;

Query Match 60.9%; Score 639.4; DB 24; Length 4960;

Best Local Similarity 75.6%; Pred. No. 2.3e-85;

Matches 793; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

QY 1 ATGCCCAAGAAGAAGAGGTGAGCAACCTGCTGACCGTGCACCAAGAACTGCCCGCC 60

Db 977 ATGCCCAAGAAGAAGAGGTGTCCAATTTACTGACCGTACACCAAAATTTGCTGCA 1036

QY 61 CTGCCCGTGGAGCCACACGACGAGGTGGCAAGAACTGATGACATGTTCCCGAC 120

Db 1037 TTACCGGTGATGCAACGAGTGTAGAGTTCGCAAGAACTGATGACATGTTCAAGGAT 1096

QY 121 CGCAGCGCTTCAGCGAGCACACCTTGGAAAGTGTCTGAGCGTGTGCCGAGCTGGGC 180

Db 1097 CGCAGCGCTTTCTGAGCATACCTGGAAAATGCTTCTCGTTTTCGCGTGTGGCGG 1156

QY 181 GCCTGTGCAAGTGAACCAACCGCAAGTGTTCCTCCCGCGAGCCGAGACGTGCCGAC 240

Db 1157 GCATGTGCAAGTTGAATTAACCGGAATGTTTCCCGAGAACCTGAAGATGTTCCGAT 1216

QY 241 TACTGTCTGCTGAGCGCCCGCGCTGGCGGTGGAAGCAATCCAGCAGCACTGGGC 300

Db 1217 TATCTTCTATATCTTTCAGCGCGCGTCTGGCAGTAAATAATATCCAGCAACATTTGGCG 1276

QY 301 CAGCTGAACATGTGCACCGCGCAGCGCGCTGCCCGCCGAGCGAGCAACGCGCTG 360

Db 1277 CAGCTGAACATGCTTCATCGTCCGGCTGCCAGCACCAAGTGACAGCAATGCTGT 1336

QY 361 AGCTGTGTGATCGCGCGCATCCGCAAGAGAACTGCAACCGCGCGAGCGCGCAAGCAG 420

Db 1337 TCACCTGTTATCGCGCGATCCGAAAGAAAGTGTGATGCGGTGAACTGCAAAACAG 1396

QY 421 GCCTGGCGCTTCAGCGCAACCGACTTCGACCGAGTGGCGAGCTGTATGAGAACAGCGAC 480

Db 1397 GCTCTAGCGTTCGAAACGCACTGATTTCCGACCAGGTTCTTCACTCATGAAAATAGCGAT 1456

QY 481 CGCTGCCAGGACATCGCAACCTGGCTTCCTGGGCGATCGCTACACACCCCTGCTGCGC 540

Db 1457 CGCTGCCAGGATATAGTAACTTGGCAATTTCTGGGGAATGCTTATACACCCCTGTACGT 1516

QY 541 ATCGCGGAGATCGCCCGCATCCGCGTGAAGGACATCAGCCGCGACCGAGCGCGCGCATG 600

Db 1517 ATAGCGGAATTCGCGAGGATCAGGGTTAAGATACTACGACTACTGACGGTGGGAAATG 1576

QY 601 CTGATCCACATCGCGCGCACCAAGACCTGTGTGAGCACCGCGCGGTGGAGAGCGCTG 660

Db 1577 TTAATCCATATTGGCAGAAACGAAACCGTGTGTAGCACCGCAGGTGTAGAGAGGCACCT 1636

QY 661 AGCCTGGGCTGACCAAGCTGTGGCGCTGGATCAGGTGAGCGGTGCGCGTGGCCGACGAC 720

Db 1637 AGCCTGGGGAACATAAATGCTGGAGCGATGGAATTCGTTCTCTGTGTGTATGATGAT 1696

QY 721 CCCAAACAACTACTGTTCTGCGCGGTGCGCAAGAACGGCGTGGCGCGCCCGCCAGCGCAC 780

Db 1697 CGAATAACTACTGTTTTCGCGGTGAGAAAATGTTGTGGCGCGCATCTGCCACC 1756

QY 781 AGCCAGCTGAGCACCGCGCGCTTGGAGGCGCATCTTTCGAGGCGCACCCACCGCTGATCTAC 840

Db |||||

Db 1757 AGCCAGCTATCAACTCGCGCCCTGGAAGGGATTTTGAAGCAACTCATCGATTGATTAC 1816

Qy 841 GGCCGACAGGACGAGCGGCGAGCGTACCTGCGCTGGAGCGGCACAGCGCCGCGTG 900

Db 1817 GGCGTAAGGATGATCTGCTGTCAGAGATACCTGGCTGCTGGACACAGTGCCTGTC 1876

Qy 901 GGCGCGCCCGCGACATCGCGCGCGCGCGCTGAGCATCCCGAGATCATCGAGCGCGC 960

Db 1877 GGAGCGCGGAGATATGGCGCGCGCTGGAGTTTCAATACCGAGATCATCAAGCTGGT 1936

Qy 961 GGCTGGACCAAGTGAACATCGTGATGAACACTACATCCGCAACCTGGACGAGACCGGC 1020

Db 1937 GGCTGGACCAATGTAATATTTGTATGAACATATATCCGTACCTGGATAGTGAACAGG 1996

Qy 1021 GCCATGTGCGCTGCTGGAGCGCGA 1049

Db 1997 GCAATGGTGGCGCTGCTGGAAGATGGCGA 2025

RESULT 8

AAD04928

ID AAD04928 standard; DNA; 5365 BP.

AC AAD04928;

XX

DT 17-JUL-2001 (first entry)

DE Retroviral vector pBABE-pgkCre used as gene trap in embryonic stem cells.

XX

KW Gene trapping construct; conditional mutation; unidirectional inversion;

KW recombinase recognition sequence; RRS; disruption cassette;

KW selection cassette; transgenic organism; retroviral vector;

KW pBABE-pgkCre; cre recombinase; phosphoglycerate kinase; PGK promoter; ds.

XX

OS Chimeric - Moloney murine leukemia virus.

OS Chimeric - Mus sp.

OS Chimeric - Bacteriophage P1.

OS Chimeric - Rhesus macaque polyoma virus.

XX

PH Key Location/Qualifiers

FT LTR 8...480

FT /*tag= a

FT /note= "5', partial MMLV U3, MMLV R and MMLV U5"

FT /partial

FT misc_feature 8...335

FT /*tag= b

FT /note= "5', partial MMLV U3"

FT /partial

FT repeat_unit 336...402

FT /*tag= c

FT /rpt_type= DIRECT

FT /note= "5', MMLV R direct repeat"

FT misc_feature 403...480

FT /*tag= d

FT /note= "5', MMLV U5"

FT misc_feature 481...1374

FT /*tag= e

FT /note= "MMLV primer binding site and extended packaging signal"

FT promoter 1417...1921

FT /*tag= f

FT /note= "Mouse phosphoglycerate kinase (PGK) promoter"

FT CDS 1972...3024

FT /*tag= g

FT /product= "Bacteriophage P1 Cre recombinase protein with a simian virus 40 large T-antigen N-terminal nuclear localisation signal"

FT promoter 3088...3168

FT /*tag= h

FT /note= "Promoter/enhancer deleted MMLV U3"

FT LTR 3187...3332

FT /*tag= i

FT /note= "3', MMLV R and MMLV U5"

FT repeat_unit /partial 3187...3253

FT /*tag= j

FT /rpt_type= DIRECT

FT /note= "3', MMLV R direct repeat"

FT misc_feature 3254...3332

FT /*tag= k

FT /note= "3', MMLV U5"

XX

FN WO200129208-A1.

XX 26-APR-2001.

XX 16-OCT-2000; 2000WO-BP10162.

XX 16-OCT-1999; 99EP-0120592.

PR 27-OCT-1999; 99US-0162016.

XX

PA (ARTE-) ARTEMIS PHARM GMBH.

PA (FRAN-) FRANKGEN BIOTECHNOLOGIE AG.

XX

PI Kuehn R, Von Melchner H, Altschmied J;

XX

DR MPI; 2001-308486/32.

XX

XX New gene trapping construct capable of causing conditional mutations in genes, comprises functional DNA segment inserted in sense or antisense direction relative to gene to be trapped -

XX

XX Example 1; Page 55-57; 78pp; English.

CC The present invention relates to a conditional gene trapping construct capable of causing conditional mutations in genes. The gene trapping construct comprises two functional DNA segments, each being flanked by two recombinase recognition sequences (RRSs) specific to site specific recombinase which is capable of unidirectional inversion of double standard DNA segment. One of the DNA segment (disruption cassette) is inserted in antisense orientation relative to the transcriptional orientation of the gene to be trapped. The other DNA segment (selection cassette) is inserted in sense direction relative to the transcriptional orientation of the gene to be trapped. The cell comprising the gene trapping construct is useful for the identification and/or isolation of genes. The transgenic organism comprising the gene trapping construct is useful to study gene function at various developmental stages. The gene trapping construct is useful for mutationally inactivating all cellular genes. The present sequence is retroviral vector pBABE-pgkCre which is used as a gene trap in embryonic stem (ES) cells. The vector pBABE-pgkCre is constructed by inserting Bacteriophage P1 cre recombinase coding region with a simian virus 40 large T-antigen N-terminal nuclear localisation signal and mouse phosphoglycerate kinase (PGK) promoter into Moloney murine leukemia virus based vector pBABEpuro.

XX

XX Sequence 5365 BP; 1208 A; 1448 C; 1402 G; 1307 T; 0 other;

Query Match 60.9%; Score 639.4; DB 22; Length 5365;

Best Local Similarity 75.6%; Pred. No. 2.3e-85;

Matches 793; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

Qy 1 ATGCCCAAGAAGAAGAGGAGGTGAGCAACCTGCTGACCGTGACCCAGAACCTGCCCGCC 60

Db 1972 ATGCCCAAGAAGAAGAGGAGGTGCTCAATTTACTGACCGTACACCAAAATTTGCTGCA 2031

Qy 61 CTGCCCGTGGAGCCACCGAGCGAGGTGCGCAAGAACTTGATGACATGTTTCGCGAC 120

Db 2032 TTACCGGTGATGCAACGAGTGATGAGGTTGCGAAGAACCTGATGACATGTTTCAAGGAT 2091

Qy 121 CGCCAGGCGCTTCAGCGAGCACACCTGGAGAGTCTGCTGAGCGTGTGCGGAGCTGGCGC 180

Db 2092 CGCCAGGCGCTTTCTTGAGCATACCTGGAAATGCTTCTGCTCGGTTTGGCGGTGGCGG 2151

Qy 181 GCCTGTGCAAGCTGAACCAACCGCAAGTGGTTCCCGCGAGCGACCGAGACCTGCGCGAC 240

Db 2152 GCATGTGCAAGTTGATTAACCGGAAATGTTTCCCGGAGAACCTGAAGATGTCGCGAT 2211

Db 1397 GCTCTAGGTTGCAACGCACTGATTTTCGACCAGGTTCTGTTCACTCATCTGGAATAATAGCGAT 1456
QY 481 CGTGCAGGACATCGCAACCTCGGCTTCTGCGCATGCGCTTCAACACACCTCTGCTCGC 540
Db 1457 CGTGCAGGATATACGTAATCTGGCATTTCTGGGATTTCTGCGGATGCTTATAACACCTCTGTACGT 1516
QY 541 ATGCGCAGATCGCCCGCATCCGCTGAGGACATCAGCCGACCGAGCGCGCGCATG 600
Db 1517 ATAGCCGAATTTGCCAGATCAGGGTTAAAGATATCTCAGTACTGACGTTGGGAGATG 1576
QY 601 CTGATCCACATCGCCCGCACCAACACCTGTGTAGCACCGCCGCGTGGAGAGCGCCCTG 660
Db 1577 TTAATCCATATTGCGAGAACGAAACACGTTGTTAGCACCGCAGGTGTAGAGAGGCACTT 1636
QY 661 AGCCTGGGCTGACCAAGCTGTGGAGCGTGTGATCAGCGTGTGAGCGCGTGGCCGAGAC 720
Db 1637 AGCCTGGGCTGAACTAAACTGGTCAGCGATGGATTTCCGCTCTCTGGTGTAGCTGATGAT 1696
QY 721 CCCAACACTACCTGTTCTGCGGCTGCGCAAGAACGCGTGGCCGCCGCCAGGCCACC 780
Db 1697 CCGAATAACTACCTGTTTTCGCGGTCAGAAAAAATGGTGTGCGCGCCATCTGCCACC 1756
QY 781 AGCCAGCTGAGCACCCCGGCTCGAGGGCATCTTCGAGGCGCACCCACCGCTGATCTAC 840
Db 1757 AGCCAGCTATCACTCGCGCTCGAAGGATTTTGAAGCACTCATGATGATTTAC 1816
QY 841 GCGCCCAAGACGACGCGGCAAGCTGCTAGCGCGTGTGAGCGGCCACAGCGCCCGCGTG 900
Db 1817 GCGCTAAGGATGACTCTGCTCAGAGATACCTGCGCTGGTCTGGACACAGTGGCCGCTGTC 1876
QY 901 GCGCCCGCCGACATGCGCGCGCGCGGTGAGCATCCCGAGATCATGAGCGCGC 960
Db 1877 GAGCGCGCGGAGATATGGCGCGCGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGGT 1936
QY 961 GGTGTGACCAACGTAACATCGTATCACTACATCCGCAACCTGGAAGACGAGACCGGC 1020
Db 1937 GGCTGGACCAATGTAATATGTTCATGAATATATATCCGTAACTGATAGTAAACAGGG 1996
QY 1021 GCATGTGCGCTGTGGAGGACGCGA 1049
Db 1997 GCAATGTGCGCTGTGGAAGATGGGA 2025

RESULT 10

AA119900
ID AAX119900 standard; DNA; 2293 BP.
XX AC AAX119900;
XX AC AAX119900;
XX DT 11-JUN-1999 (first entry)
XX DE Plasmid pOG304M containing mp1 promoter and Cre coding sequences.
XX KW Mouse; mp1; promoter; site-specific recombination; Cre recombinase;
XX KW protamine 1; fusion gene; transgenic mouse; ss.
XX OS Synthetic.
XX OS Mus musculus.
XX PN WO9910488-A1.
XX PD 04-MAR-1999.
XX PF 28-AUG-1998; 98WO-US17852.
XX PR 28-AUG-1997; 97US-0919501.
XX PR (SALK) SALK INST BIOLOGICAL STUDIES.
XX PI O'Gorman S, Wahl G;
XX PR WPI; 1999-190617/16.

PT New nucleic acid construct, comprising a germline-specific promoter
PT operably linked to a recombinase coding sequence - useful for
PT producing subtle, conditional or tissue-specific mutations
XX
PS Example 1; Page 48; 54pp; English.
XX

CC The present invention describes a nucleic acid construct, comprising a
CC germline-specific promoter operably linked to a recombinase coding
CC sequence. The construct can be useful for modulating agronomic
CC characteristics, including (a) biotic stress tolerance, increased
CC resistance to herbicides, pest damage, and viral, bacterial, and fungal
CC diseases, improvement of crop nutritional quality, reduction of
CC post-harvest losses, improved quantity and composition of endogenous
CC products, and production of new plant-derived compounds. The
CC production of alleles containing single recombinase target sites and a
CC desired mutation are useful for producing subtle and conditional
CC mutations that require generation of alleles with minimal structural
CC alterations. They are also useful for generating null alleles.
CC mp1-mediated nucleic acid constructs are useful for producing embryos
CC containing genetically lethal alleles. The recombinase constructs are
CC expressed at high levels in the germ line, but not to a functionally
CC significant degree in ES cells or embryonic or adult somatic tissue.
CC This enables modulation of recombined target nucleic acid sequences in
CC the early embryo. In addition, tissue-specific and conditional
CC recombinatory tools permit the generation of transgenic plants and
CC animals. The present sequence represents a plasmid containing mouse
CC protamine 1 promoter and Cre coding sequences from an example of the
CC present invention.

SQ Sequence 2293 BP; 555 A; 559 C; 603 G; 576 T; 0 other;

Query Match 60.6%; Score 636.4; DB 20; Length 2293;
Best Local Similarity 75.5%; Pred. No. 6.8e-85;
Matches 790; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

QY 4 CCCAAGAAGAGGAGGTGAGCAACCTGCTGACCGTGCACAGAACCTGCGCCCTG 63
Db 699 CCCAAGAAGAGGAGGTGCTCAATTTACTGACCGTACACCAAAATTTGCTGCATTA 758
QY 64 CCGTGGACGCCACCGACGAGGTGCGCAAGACCTGATGACATGTTCCGCGACCGC 123
Db 759 CCGTGCATGCAACGAGTATGAGGTTGCGAAGACCTGATGACATGTTCCAGGATCGC 818
QY 124 CAGGCTTCAGCGAGCACACCTGGAAGATGCTGCTGAGCGTGTGCCGACAGTGGCGCGC 183
Db 819 CAGGCTTTCTGAGCATACCTGGAAATGCTTCTGCTCGTTGCCGCTGTTGGGCGGCA 878
QY 184 TGGTGAAGCTGAACACCGAAGTGGTTCGCCGCGAGCCCGAGACGTCGCGCATC 243
Db 879 TGGTGAAGTTGAATAACCGGAAATGGTTTCCCGCAGAACCTGAAGATGTTCCGATAT 938
QY 244 CTGCTGTACTGTCAGGCGCGCGCTGGCGGTGAAGACCATCCAGCAGCACCTGGGCGCAG 303
Db 939 CTTCATATCTTCAGCGCGCGGTCTGGCAGTAAATACTATCCAGCAATTTGGGCGCAG 998
QY 304 CTGAACATGCTGCACCGCGCAGCGCTGCGCCGCCCGCCAGCAGCAACCGCTGAGC 363
Db 999 CTAAACATGCTTTCATGCTCGGTCCGGGTGCCAGCACCAAGTGACAGCAATGCTGTTCA 1058
QY 364 CTGGTGTATGCGCGCATCCGAGAGAACCTGAGCGCGCGGCGAGCGCGCCAGCGGC 423
Db 1059 CTGGTGTATGCGCGCATCCGAAAGAAACGTTGATGCGCGGTGAACGCTGCAAAACAGGCT 1118
QY 424 CTGGCTTCAGCGCACCGACCTTCGACCAAGTGGCGAGCTCATGAGAGAACCGCACCGC 483
Db 1119 CTAGCGTTCGAACGCACTGATTTGACAGGTTGTTCTACTCATGGAATAGCGATCGC 1178
QY 484 TGCCAGGACATCCGCAACCTGCGCTTCTCTGGGCATCGCTCAACACACCTGCTGGCGATC 543
Db 1179 TGCCAGGATATACGTAATCTGCAATTTCTGGGATGCTTTATAACACCTGTTACGTATA 1238
QY 544 GCGGAGATCGCCGATCGCGTGAAGGACATAGCCGCGACCGAGCGCGCGCATGCTG 603

```
Db 1239 GCCGAAATGCCAGGATCAGGGTTAAAGATATCTCACGTACTGACGGTGGGAGATGTTA 1298
QY 604 ATCCACATCGCCCGCCACCAAGACCTCGTGTAGACCGCCGCGTGGAGAGCCCTGAGC 663
Db 1299 ATCCATATGGCAGAAAGAAACCTCGTTAGCACCGCAGCGTGTAGAGAGGCACTTAGC 1358
QY 664 CTGGCGGTGACCAAGCTGGTGGAGCGCTGGATCAGCGGTGAGCGCGTGGCGGACGCC 723
Db 1359 CTGGGGTAACTAAACTGGTTCGACGATGGATTTCCGTTCTGTGTAGCTGATGATCCG 1418
QY 724 AACAACTACCTGTTCTGCGCGTGCAGCAAGACCGCGTGGCGGCCCGCCAGCCACCAGC 783
Db 1419 AATAACTACCTGTTTTCGCGGTGAGAAATAATGTTGTGCGCGCATCTGCCACCAGC 1478
QY 784 CAGCTGAGCACCGCGGCTGGAGGATCTTCGAGCGACCAACCGCTGATCTAGCGC 843
Db 1479 CAGCTCACTACGCGCGCTGGAGGGATTTTGAAGCAACTCATCGATTGATTTACGGC 1538
QY 844 GCCAAGACACAGCGCGCAGCGCTACTCGCTGGAGCGGCCACAGCGCCCGGTGGGC 903
Db 1539 GCTAAGATGACTGTGTGAGATACCTGGCCCTGGTCTGGACACATGCCCCGTGCGA 1598
QY 904 GCCGCCCGGACATGGCCCGCGCGGTGAGCATCCCGAGATCATCGAGCGCGCGGC 963
Db 1599 GCGCGCGAGATATGCCCGCGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGGTGC 1658
QY 964 TGGACCAACGTGAACATGATGTAACATCATCGCGAACCCTGGACAGCAGACCGCGCC 1023
Db 1659 TGGACCAATGTAATATTTGTCATGAACATATATCCGTAACCTGGATAGTGAACAGGGCA 1718
QY 1024 ATGCTGCGCTGCTGGAGGAGCGCA 1049
Db 1719 ATGGTGCCTGCTGGAGATGGCGA 1744
```

RESULT 11

AAH26331

ID AAH26331 standard; DNA; 5261 BP.

XX

AC AAH26331;

XX

DT 02-OCT-2001 (first entry)

XX

DE Recombinant adenovirus delta-E1 Cre-LoxP Ad.

XX

KW Adenovirus; delta-E1 Cre-LoxP Ad; adeno-associated virus; vector;

XX

KW gene therapy; ds.

XX

OS Chimeric - Mastadenovirus.

OS

OS Chimeric - Human cytomegalovirus.

OS

OS Chimeric - Rhesus macaque polyoma virus.

XX

FH Key Location/Qualifiers

FT promoter

FT 551..1186

FT /*tag= a

FT /note= "CMV promoter"

FT polyA_site

FT 2251..2476

FT /*tag= b

FT /note= "SV40 polyA site"

FT 2476..2520

FT /*tag= c

FT /function= "loxP site"

XX

PN W0200155361-A2.

XX

XX 02-AUG-2001.

XX

XX 26-JAN-2001; 2001WO-US02709.

XX

XX 26-JAN-2000; 2000US-0178536.

XX

XX (CHIR) CHIRON CORP.

XX

PI Hardy SP;

XX

XX WPI; 2001-483239/52.

XX

Producing recombinant adeno-associated virus (rAAV) vector, by stably infecting eukaryotic host cell with rAAV vectors, helper adenovirus or herpes virus, recombinant adenovirus or herpes vectors -

XX

PS Disclosure; Page 60-62; 63pp; English.

XX

The present sequence is that of recombinant adenovirus delta-E1 Cre-loxP Ad, in which the E1 gene of the wild-type adenovirus is substituted by plasmid DNA comprising a cytomegalovirus (CMV) promoter inserted immediately downstream of the CMV promoter followed by a sequence from SV40 that specifies polyadenylation in mRNA, and a loxP site. The recombinant adenovirus is used as an induction system in methods of the invention. Thus, methods and compositions are provided for producing recombinant adeno-associated virus (rAAV) vector particles by: (a) introducing into a host cell (i) AAV packaging plasmid pflxAAV (see AAH26332), (ii) a recombinant viral vector encoding plasmid, and (iii) a plasmid encoding herpesvirus, cytomegalovirus or adenoviral functions, or a herpesvirus, cytomegalovirus or adenovirus itself, to produce a flox AAV particles and rAAV particles; and (b) introducing into a second host cell (i) the rAAV particles or (a), (ii) a vector that directs expression of Cre, and (ii) a vector which directs expression of herpes virus, cytomegalovirus or adenovirus helper functions, such that rAAV vector particles are produced. The vectors are useful for in vivo or in vitro gene therapy and also for in vitro recombinant protein production.

XX

SQ Sequence 5261 BP; 1309 A; 1238 C; 1329 G; 1385 T; 0 other;

Query Match 60.0%; Score 630; DB 22; Length 5261;

Best Local Similarity 75.1%; Pred. No. 5.4e-84;

Matches 786; Conservative 0; Mismatches 260; Indels 0; Gaps 0;

```
QY 4 CCCAAGAAGAGGAGGTGAGCAACCTGCTGACCGTGACACCGACCTGCGCGCCCTG 63
Db 1201 CCAAGAAGAAGAGGAGGTTCGAATTTACTACCGGTACACCAAAATTTGCCGTG 1260
QY 64 CCGTGTGAGCCACCGACGAGGTGCGCAGAGCTGCGCAGAACTGATGACATGTTCC 133
Db 1261 CCGGTGATGCAACGAGTGATGAGGTTTCGCAAGAACTGATGACATGTTTCAGG 1320
QY 124 CAGCGCTTCAGCGAGCACACCTCGAAAGATGCTCTGAGCGTGTGCCGAGCTGG 183
Db 1321 CAGCGCTTTCTGAGCATACCTGGAAATGCTTCTGCTCGTTTCCGGTCTGGGG 1380
QY 184 TGGTGAAGCTGAACCAACCGCAAGTGGTTCGCCGCGAGCCGAGGACGTCGCGA 243
Db 1381 TGGTGAAGTTGAATTAACCGGAAATGGTTTCCCGCAGAACCTGATGACATG 1440
QY 244 CTGCTGTACTCTGAGCGCCGCGCTGGCGGTGAAGACCATCCAGCAGACCTGG 303
Db 1441 CTTCTATATCTTCAGCGCGCGGTCTGGCAGTAAAAAATATCCAGCAACATTT 1500
QY 304 CTGAACATGTGCACCGCGCAGCGCCTGCGCCGCCCGCCAGCAGCAACGCGTG 363
Db 1501 CTAAACATGTTTCATGTCGGTCCGGGTGCCAGGACCAAGTGACAGCAATG 1560
QY 364 CTGGTGAATGCGCGCATCCGCAAGGAGAACGTGGACCGCGCGAGCGCCGCAAG 423
Db 1561 CTGGTTATGCGCGGATCCGAAAGAGAAACGTTTGAATGCGCGGTGAACGTG 1620
QY 424 CTGGCCTTCGAGCGCACCGACTTCGACGAGGTGCGGACCTGATGAGAGAACG 483
Db 1621 CTAGCGTTCGAACGCACTGATTCGACCGAGGTTCTGTTCACTCATGGAATA 1680
QY 484 TGCAGGACATCGCAACCTGCGCTTCCTGGGCGATCGCTTACAAACCTGTCG 543
Db 1681 TGCCAGGATATAGTAACTTCTGGGATTTCTGGGATTTGCTTATAACCCCTG 1740
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QY 544 GCCGAGATCGCCGATCCGGTGAAGACATCAGCCGACCGACCGCGCGCGCGCATCTG 603
Db 1741 GCCGAAATTCAGAGTACAGGTTAAAGATATCTCAGTATCTGACGGTGGAGAAATGTTA 1800
QY 604 ATCCACATCGCCGACCAAGACCTCGTGAGACACCGCGCGTGGAGAGGCCCTGAGC 663
Db 1801 ATCCATATTGGCAGAACGAAACCGTGGTTAGACCCGAGGTGTAGAGAGGCACATTAGC 1860
QY 664 CTGGCGGTGACCAAGCTGGTGGAGCGCTGGATCAGCTGAGCGCGTGGCCGACGACCCC 723
Db 1861 CTGGGGGTAACTAAACTGGTTCGAGCGATGGATTTCCGCTCTCTGGTGTAGCTGATCCG 1920
QY 724 AACCACTACCTGTTCTCGCGGTGCGCAAGACCGCGTGGCGCCCGCCAGCGGCACGAC 783
Db 1921 AATAAATACCTGTTTTCGCGGTGAGAAATGTTGTCGCGCGCATCTGCGCACGAC 1980
QY 784 CAGCTGAGCACCGCGGCTGGAGGGCATCTTCAGGCGCACCCACCGCTGATCTAGCGC 843
Db 1981 CAGTATCAACTCGCGCTGGAGGGATTTTGAAGCAACTCATCGATTGATTAGCGC 2040
QY 844 GCCAAGACGACGCGCGAGCGTACTCTGCGCTGGAGCGGCCACAGCGCCCGCGTGGC 903
Db 2041 GCTAAGGATGACTCTGGTTCAGAGATACCTGCGCTGGTCTGACACAGTGGCCGTCGGA 2100
QY 904 GCGCCCGGACATGCGCGCGCGCGGTGAGCATCCCGAGATCATGCGAGCGCGCGC 963
Db 2101 GCGCGCGGAGATGCGCGCGCGCTGGAGTTTCAATACCGGAGATCATGCAAGTGGTGGC 2160
QY 964 TGGACCAACGTGAACATCGTGATGAACCTATACCGCAACCTGGACAGCGAGACCGCGGCC 1023
Db 2161 TGGACCAATGTAATATTGTTCATGAACCTATATCCGTAACCTGATGTAAGAGGGGCA 2220
QY 1024 ATGTTGCGCTGCTGGAGGAGCGGA 1049
Db 2221 ATGTTGCGCTGCTGGAAGATGGGA 2246
```

RESULT 12

AAC62541
ID AAC62541 standard; DNA; 1172 BP.

AC AAC62541;

DT 07-FEB-2001 (first entry)

XX Cre wild-type coding sequence.

XX Cre variant recognition site; lox site; recombinase;

XX variant recombination site; hybrid crop production; seedless crop;

XX phage packaging; cloning; ds.

OS Unidentified.

XX WO2000060091-A2.

XX 12-OCT-2000.

XX 06-APR-2000; 2000WO-US09154.

XX 06-APR-1999; 99US-0127977.

XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.

XX Sauer BL, Rufer AW;

XX WPI; 2000-665010/64.

XX Identifying variant recombinases mediating recombination at variant
PT sites (vrs) by contacting a mutant recombinase, a first and second vrs
PT having a reporter gene, and a second nucleic acid having 2 vrs and a
PT reporter gene -

PS Example 1; Page 98-101; 144pp; English.

XX

CC The present invention relates to the identification of recombinase
CC variants which have an altered specificity. They are tested using
CC constructs containing variant recognition sites, which are not recognised
CC by non-mutant recombinase but undergo recombination in the presence of a
CC variant enzyme. Variant recombinases are useful in the production of a
CC genetically modified crop plants, particularly seedless varieties, and in
CC phage packaging, which has uses in cloning.

XX SQ Sequence 1172 BP; 299 A; 263 C; 323 G; 287 T; 0 other;

Query Match 59.2%; Score 621.8; DB 21; Length 1172;

Best Local Similarity 74.5%; Pred. No. 1e-82;

Matches 782; Conservative 0; Mismatches 267; Indels 0; Gaps 0;

QY 1 ATCCCCAAGAAGAGGAGGTGAGCAACCTCTGACCGTGACACAGAACCTGCCCGCC 60

Db 35 ATCCTCTAGACTGAGTGTGAATGTCCAATTTACTGACCGTACACCAAAATTTGCTGCA 94

QY 61 CTGCGCGTGAACGCCACCGACGAGGTGCGCAAGAACTGATGACATGTTTCCCGGAC 120

Db 95 TTACCGGTGATGCAACGAGTGTGATGAGTTTCGCAAGAACTGATGACATGTTTCAGGGAT 154

QY 121 CGCCAGGCTTCAGCGAGCACACCTGGAAGATGCTGCTGAGCGTGTGCCGACTGGGCC 180

Db 155 CGCCAGCGTTCGAGCATACCTGGAATAATGCTTCTGTCGGTTTGCCTGCTGCGCG 214

QY 181 GCCTGCTGAAGCTGAACCAACCGCAAGTGTTCCTCCCGCGAGCCCGAGGACGTTGCCGAC 240

Db 215 GCATGCTGAAGTTGAATTAACCGGAATGTTTCCCGAGAACCTGAAGATGTTCCGAT 274

QY 241 TACTGCTGTACTCTGAGGCGCGCGCTGCGCGTGAAGACCATTCAGAGCACCTTGGGC 300

Db 275 TATCTTCTATCTTCAGGCGCGCTGTCGAGTAAATAATATCCAGCAACATTTGGGC 334

QY 301 CAGCTGAACATGCTGACCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360

Db 335 CAGCTAAACATGCTTCATGCTCGGCTCCGCGCTCCACGACCAAGTACAGCAATGCTGT 394

QY 361 AGCTGCTGATGCGCGCATCCCGAAGAGAACTGGAAGCGCGCGCGCGCGCGCGCGCG 420

Db 395 TCACTGTTATGCGCGGATCCGAAAGAAAGAAAGTTGATGTCGCGTGAACGTGCANAACAG 454

QY 421 GCGTGGCGCTTCAGAGCGCACCTTCGACCGAGTGGCGAGCGCTGATGAGAGAACAGGAC 480

Db 455 GCTCTAGCGTTCGAACGCACTGATTTTCGACCAAGTTCGTTTCACTCATGGAATAAGCAT 514

QY 481 CGCTGCGAGACATCCGCAACCTGCGCTTCCTGGGATCGCTTACCAACACCTGCTGCGC 540

Db 515 CGCTGCGAGATATAGTAACTTGGCATTTCTGGGATGCTTATTAACCCCTGTTACGT 574

QY 541 ATCGCGGATCGCCCGCATCCCGTGAAGGACATCAGCGCGACCGCGCGCGCGCGCGCATG 600

Db 575 ATAGCGAAATTCAGAGGATCAGGGTTAAAGATATCTCAGTACTACGCTGGGGAATG 634

QY 601 CTGATCCATATCGCGCGCACCAAGACCTGCTGTGAGCACCGCGCGCTGAGAGAGCGCTG 660

Db 635 TTAAATCCATATTGGCAGAAACGCTGGTTAGCACCGCGAGGTGTAGAGAGGACATT 694

QY 661 AGCTGCGGTGACCAAGCTGGTGGAGCGCTGATCAGCGTGGAGCGCGTGGCGCGGAC 720

Db 695 AGCTGGGGTAATTAACCTGTCGAGCGATGATTTCCGTTCTCTGTGTAGCTGATGAT 754

QY 721 CCGAATAACTACCTGTTTCCCGGTGCGCAAGAAAGCGGTGTGCGCGCGCGCGCGCAC 780

Db 755 CCGAATAACTACCTGTTTCCCGGTGCGCAAGAAAGCGGTGTGCGCGCGCGCGCGCAC 814

QY 781 AGCAGCTGAGCACCGCGCGCTGAGGCGCATCTTCAGAGCGCACCAACCGCGCTGATCTAC 840

Db 815 AGCAGCTATCAACTCGCGCGCTGGAAGGGAATTTTGAAGCAACTCATCGATTGATTAC 874

QY 841 GCGCGCAAGGACGACGCGCGCGCTACCTGCGCTGGAGCGCGCGCGCGCGCGCGCG 900

Db 875 GGGCTAAGGATGACTCTGCTCAGAGATACCTGGSCCTGGTCTGGACACAGTGCCTGGTC 934
 QY 901 GGGCCGCCCGCGACATGGCCCGCGGCTGAGCATCCCGAGATCATGCGAGCGCGC 960
 Db 935 GGAGCCGCGGAGATATGGCCCGGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGGT 994
 QY 961 GGCTGGACCAACGTGAACATCGTGATGAACCTACATCCGCAACCTGGACAGCGAGCCGGC 1020
 Db 995 GGCTGGACCAATGTAATATTGTCATGAATATATCCGTAACTTGGTAACTGGATAGTGAACAGGG 1054
 QY 1021 GCCATGCTGGCCCTGCTGGAGGACGGCA 1049
 Db 1055 GCAATGCTGGCCCTGCTGGAGATGGCA 1083

RESULT 13

ABN97179

ID ABN97179 standard; DNA; 1553 BP.

XX AC ABN97179;

XX 13-AUG-2002 (first entry)

DT Gene #3677 used to diagnose liver cancer.

DE Gene: liver cancer; ds; hepatocellular carcinoma; hepatotropic;
 KW metastatic liver tumour; cytostatic; expression profile; disease state;
 KW disease progression; drug toxicity; drug efficacy; drug metabolism.

XX Homo sapiens.

XX W0200229103-A2.

XX 11-APR-2002.

XX 02-OCT-2001; 2001WO-US30589.

XX 02-OCT-2000; 2000US-237054P.

XX (GENE-) GENE LOGIC INC.

XX Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;

XX WFI; 2002-426119/45.

XX Diagnosing and detecting the progression of liver cancer,
 PT hepatocellular carcinoma or metastatic liver tumor in a patient,
 PT involves detecting the level of expression of two or more genes in a
 PT liver tissue sample

XX Claim 1; SEQ ID NO 3677; 298pp; English.

XX The invention relates to a novel method for diagnosing and detecting the
 CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
 CC tumor in a patient, and differentiating metastatic liver cancer from
 CC hepatocellular carcinoma in a patient, involving detecting the level of
 CC expression of two or more genes represented in ABN97455 in a
 CC tissue sample. The method of the invention has hepatotropic, and
 CC cytostatic activity. The method is useful for diagnosing and detecting
 CC the progression of liver cancer, hepatocellular carcinoma and metastatic
 CC liver carcinoma in a patient. The method is useful for identifying
 CC expression profiles which serve as useful diagnostic markers as well as
 CC markers that can be used to monitor disease states, disease progression,
 CC drug toxicity, drug efficacy and drug metabolism.

CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences.

XX SQ Sequence 1553 BP; 424 A; 340 C; 394 G; 395 T; 0 other;

Query Match

Best Local Similarity 58.9%; Score 618.4; DB 24; Length 1553;

Matches 775; Conservative 0; Mismatches 261; Indels 0; Gaps 0;

QY 14 AGAGGAAGGTGAGCAACCTGCTGACCGTGACACAGAACTGCCCCGCTGCCCGTGGACG 73
 Db 477 AGTGTTAAATGTCCAAATTTACTGACCGTATACCAAAATTTGCTGCAATTACCGGTGATG 536
 QY 74 CCACCAAGCAGCAGGCTGCGCAAGAACTCTGATGACATGTTCCGCGACCGCCAGGCTTCA 133
 Db 537 CAACGAGTGATGAGGTTCCGCAAGAACCTGATGACATGTTTCAGGATTCGCGAGCGTTT 596
 QY 134 GCGAGCACACCTGGAAAGATGCTGCTGAGCGTGTGCGCGAGCTGGCGCGCTGGTCAAGC 193
 Db 597 CTGAGCATACCTGGAAATGCTTCTGCTCCGTTTGCCTGCTGGCGGATGGTGAAGT 656
 QY 194 TGAACAAACCGCAAGTGGTTCCCGCCGAGCCCGAGGACGTGCGCGACTACCTGCTGTACC 253
 Db 657 TGAATAACCGGAAATGGTTTCCCGCAGAACTCTGAAGATGTTGCGGATTATCTTCTATATC 716
 QY 254 TGCAGGCCCGCGCTGGCGCTGGAAGACCATCCAGCAGACACCTGGCGCGAGCTGAACATGC 313
 Db 717 TTCAGCGCGCGCTCTGGCAGTAAAACTATCCAGCAACATTTGGGCCAGCTAAACATGC 776
 QY 314 TGCACCGCCGACGCGCTTGCCTCCGCCGCCAGCGACAGCAACGCGCTGAGCTGGTATGC 373
 Db 777 TTCATGCTCGTCCGGCTGCCAGCAAGTGACAGCAATGCTGTTTCACTGGTTATGC 836
 QY 374 GCGCATCCGCAAGGAGAACGTGGAGCCGCGGAGCGCGCCAGCAAGCGCCCTGGCCTTCG 433
 Db 837 GCGCGATCCGAAAGAAAAACGTTGATGCCGCTGAACTGCAAAACAGAGGCTCTAGCCTTCG 896
 QY 434 AGCGCACCGACTTTCGACACAGGTGCGCAGCTGATGAGAACAGCAGCAGCCGCTGCCAGACA 493
 Db 897 AACGCACTGATTTGACCAAGGTTGTTTCACTCATGGAATAATAGCGATTCGCTGCCAGATA 956
 QY 494 TCCGCAACCTGGCTTCTTGGGCTATCGCTTAAACACCTGCTGCCCATCGCGAGATCG 553
 Db 957 TAGGTAATCTGGCAATTTCTGGGGATTGCTTATAACACCTCTTACGTATAGCCGAATTG 1016
 QY 554 CCGCATCCGCGTGAAAGGACATCAGCCGCAACGAGCGCGCGCATGCTGATCCACATCG 613
 Db 1017 CCAGGATCAGGGTTAAAGATATCTCAGCTACTGACGGTGGGAGATGTTAAATCCATATTG 1076
 QY 614 GCGCACCAAGACCTGCTGAGCACCGCGCGGTGGAGAAAGCCCTGAGCCTGGGCGTGA 673
 Db 1077 GCAGAAACGAAACCGCTGGTTAGCACCGCAGGTGTAGAGAAAGGCACCTTAGCCTGGGGTAA 1136
 QY 674 CCAAGCTGTGGAGCGCTCGATCAGCGTGAGCGCGCTGCGCGACACCCCAACAACTACC 733
 Db 1137 CTAACTGTGTCGAGCGATGGAATTTCCGTCTCTGCTGTAGTGTATCGAATACTACC 1196
 QY 734 TGTTCTGCGCGTGCGCAAGAACGGCGTGGCGCCCCCAGCGCCACCCAGCCAGCTGAGCA 793
 Db 1197 TGTTTTCGCGGGTTCAGAAAAATGGTGTTCGCGCGCATCTGCCACAGCCAGCTATCAA 1256
 QY 794 CCGGGCCCTGGAGGCGATCTTCGAGGCCACCCACCGCTGATCTACGGCGCCCAAGGACG 853
 Db 1257 CTGCGCCCTGGAAGGGATTTTGAAGCAACTCATCGATTGATTACGGCGCTAAGGATG 1316
 QY 854 ACAGCGCCGAGGCTACCTGGGCTTGAGCGGGCCACAGCGCCCGCGTGGCGCGCCCGCG 913
 Db 1317 ACTCTGTCAGAGATACCTGGCTGTCTGGACACAGTGCCTGTCGAGCGCGCGCGAG 1376
 QY 914 ACATGCGCGCGCGCGTGAAGATCCCGAGATCATCCGAGATCATGAGCGCGCGCTGACCAACG 973
 Db 1377 ATATGCGCGCGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGGTGGCTGGACCAATG 1436
 QY 974 TGAACATCGTGATGAATACATCCGCAACTCGACAGCAGACCGCGCGCATGTGCGCC 1033
 Db 1437 TAAATATTGTCATGAATATATCCGTAACTAGTAGTGAAGCAAGGGGAATGGTGGCGC 1496
 QY 1034 TGCTGGAGGACGCGCA 1049
 Db 1497 TGCTGGAGATGGCGA 1512

RESULT 14
 AAD35276
 ID AAD35276 standard; DNA; 1553 BP.
 XX
 AC AAD35276;
 XX
 DT 25-JUL-2002 (first entry)
 XX
 DE Bacteriophage P1 Cre recombinase DNA.
 XX
 KW Site-specific DNA recombinase; DR1; membrane translocation sequence; MTS;
 KW cell-permeable recombinase; nuclear localisation signal; NLS; excretion;
 KW trafficking; blood-brain barrier; gene; ds.
 XX
 OS Bacteriophage P1.
 XX
 PN W020020737-A2.
 XX
 PD 14-MAR-2002.
 XX
 PF 07-SEP-2001; 2001WO-US28209.
 XX
 PR 07-SEP-2000; 2000US-230690P.
 XX
 PA (UYVA-) UNIV VANDERBILT.
 XX
 PI Ruley HE, Jo D;
 XX
 DR WPI; 2002-362248/39.
 XX
 PT New isolated polypeptide comprising a cell-permeable site-specific DNA
 PT recombinase and membrane translocation sequence for stimulating
 PT site-specific DNA recombination in a cell -
 XX
 PS Example 1; Page 66-67; 70pp; English.
 XX
 CC The invention relates to a polypeptide comprising a site-specific
 CC DNA recombinase (DR1) and a membrane translocation sequence (MTS),
 CC and nucleic acids that encode such cell-permeable recombinases. The
 CC sequences of the invention are useful for stimulating site-specific
 CC DNA recombination in a cell and for determining the efficiency of
 CC protein transduction into a population of cells. The polypeptide of
 CC the invention is further useful for detecting whether site-specific
 CC DNA recombination has occurred within a cell and for identifying a
 CC compound that modulates nuclear metabolism in a cell. It is used for
 CC identifying a peptide that behaves as a membrane translocation or
 CC nuclear localisation signal (NLS) and is also useful for identifying
 CC a compound preferably an amino acid sequence that modulates the
 CC delivery of a polypeptide to a cell or the activity of a polypeptide
 CC in a cell, where the compound modulates trafficking, uptake, excretion
 CC or other activity of a specific therapeutic protein, by enhancing
 CC protein delivery across the blood-brain barrier. The present sequence
 CC is Bacteriophage P1 Cre recombinase DNA.
 XX
 SQ Sequence 1553 BP; 424 A; 340 C; 394 G; 395 T; 0 other;

Query Match 58.9%; Score 618.4; DB 24; Length 1553;
 Best Local Similarity 74.8%; Pred. No. 3.1e-82;
 Matches 775; Conservative 0; Mismatches 261; Indels 0; Gaps 0;

QY 14 AGAGGAGGTGAGCAACCTGCTGACCTGACCGTACACGAACTGCGCGCCCTGCCGTGGACG 73
 DB 477 AGTGTAAATGTCCAAATTTACTGACCGTACACCAAAATTTGCGCTGCATTACCGGTGATG 536
 QY 74 CCACGACGAGGTGCGAAGAACCTGATGGACATGTTCCGGACCGCGACGCGCTTCA 133
 DB 537 CAACGATGATGAGTTGCGAAGAACCTGATGGACATGTTGAGGATCGCAGCGGTTTT 596
 QY 134 GCGAGCACCTGGAAGATGCTGCTGAGCGTGTGCCGACGTGGCGCGCTGTGTGAAGC 193
 DB 597 CTGAGCATACCTGGAATAATGCTTCTGTCCGTTTTCGCGGTGTGGCGGCGATGTGCAAGT 656

QY 194 TGAACCAACCGCAAGTGGTTCCCGCGGAGCCCGAGAGCGTGGCGACTACCTGCTGTACC 253
 DB 657 TGAATAACCGGAATGGTTTCCCGCAGAACCTGGAAGATGTTCCCGATTATCTTCTATATC 716
 QY 254 TGCAGGCCCGCGCTGCGGTGAAGACCATCAGCAGCACCTGGCGCAGCTGAACATGC 313
 DB 717 TTCAGGCGCGGTCTGGCAGTAAAACTATCCAGCAATTTGGGCGAGCTAAACATGC 776
 QY 314 TGCACGCGCGAGCGCTTGCCTCCCGCCAGCGACAGCAACCGCTGAGCCCTGGTGAATC 373
 DB 777 TTCACTCGTCCGTCGCGCTGCCACGACCAAGTACAGCAATGCTGTTTCACTGGTTATGC 836
 QY 374 GCGCATCCGCAAGAGACGTGGACGCGCGGAGCGCGCCCAAGCAGGCGCTGGCCTTCG 433
 DB 837 GCGGATCCGAAAGAAACGTTGATGCGCGTGAACGTGCAAAACAGGCTCTAGCGTTTCG 896
 QY 434 AGCGACCGACTTTCGACCAAGTGCAGCCTGATGGAGAACAGCACCGCTGCCAGGACA 493
 DB 897 AACGCACTGATTTCCGACGAGTTGTTCACTCATGGAAATAGCGATCGTCCAGGATA 956
 QY 494 TCGCAACCTGCGCTTCTGGGCGATGCGCTACAACACCTGTGTGGCATCGCGAGATCG 553
 DB 957 TACGTAATCTGGCAATTTCTGGGGAATGCTTATAACACCTGTTACGTATAGCGAAATG 1016
 QY 554 CCGCATCCGCTGAAGGACATCAGCGCACCGCGCGCGCGCGCATGCTGATCCACATCG 613
 DB 1017 CCAGGATCAGGTTAAAGATATCTCACGTACTGACGCTGGGAGAATGTTAATCCATATTG 1076
 QY 614 GCGCACCAAGACCTTGTGTGAGCACCGCGCGGTGGAGAAAGCCCTGAGCCTGGGCGTGA 673
 DB 1077 GCAGAACGAAACGCTGTTAGCACCGCAGGTGTAGAGAAAGCACTTAGCCTGGGGTAA 1136
 QY 674 CCAAGCTGTGAGCGCTCGATCAGGTGAGCGGTGGCGCGAGACGACCCCAACACTAC 733
 DB 1137 CTAAACTGTGCGAGCGATGGAATTTCCGTCTCTGGTGTAGCTGATGATCCGAATAACTAC 1196
 QY 734 TGTCTGCGCGTGGCGAAGAACGGCGTGGCGCGCCCGCCAGCGCCACCGAGCTGAGCA 793
 DB 1197 TGTTTTGCGGGTTCAGAAAAATGTTGTCGCGCCATCTGCCACCGACCGAGCTATCAA 1256
 QY 794 CCGCGCCCTGAGAGGCATCTTCGAGGCCACCCACCGCTGATCTACGCGCGCAAGGACG 853
 DB 1257 CTCGCGCTTGAAGGATTTTGAAGCAACTCATCGATTGATTACGGCGCTAAGATG 1316
 QY 854 ACAGCGCGCAGCGCTACCTGCGCTGAGCGGCGCACAGCCCGCGTGGCGCGCCCGCG 913
 DB 1317 ACTCTGTCAGAGATACCTTGGCTGTGTCGACACAGTCCCGTGTGCGAGCGCGCGAG 1376
 QY 914 ACATGCGCGCGCGGTGAGCATCCCGAGATCATGCGCGCGCGCTGACCCCAACG 973
 DB 1377 ATATGCGCGCGGTGGAGTTTCAATACCGAGATCATGCAAGCTGTGTGACCAATG 1436
 QY 974 TGAACATCGTGAATCACTACATCCGCAACTCGACAGCGAGACCGCGCGCATGTTGCGCC 1033
 DB 1437 TAAATATTGTCATGAATATATCCGTAACTCGATAGTAGTAACAGGCGCAATGGTTCGCC 1496
 QY 1034 TGCTGAGGACGCGA 1049
 DB 1497 TGCTGAGATGCGCA 1512

RESULT 15
 ABK10252
 ID ABK10252 standard; DNA; 1553 BP.
 XX
 AC ABK10252;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE Bacteriophage P1 Cre site specific recombinase gene.
 XX
 KW Transgenic plant; site-specific recombinase; transgene excision;
 KW Cre; Cre/Lox; DNA excising gene cassette; ds.

XX Bacteriophage P1.
OS WO200210415-A2.
PN 07-FEB-2002.
XX
XX 27-JUL-2001; 2001WO-US23794.
XX
XX 28-JUL-2000; 2000US-221318P.
PR (UYCO-) UNIV CONNECTICUT.
XX
XX Li Y, O'donnell CP, Duan H, Wu YH, Mcavoy R;
XX WPI; 2002-217124/27.
DR
XX
XX Creating a transiently transgenic plant for producing non-transgenic
PT food products, comprises introducing a gene cassette having
PT multifunctional transgenic DNA sequences which excise themselves from
PT the genome -
XX
PS Example 1; Page 51; 58pp; English.
XX
CC This invention relates to a novel method for creating a transiently
CC transgenic plant. The method comprises introducing a gene cassette
CC containing transgenic gene sequences conferring a desirable phenotypic
CC trait, a recombinase-type protein, sequences cleavable by a recombinase
CC protein and a promoter to a plant. The plant is then exposed to a
CC stimulus that activates the promoter and directs expression of the
CC recombinase protein which excises the heterologous DNA from the plant
CC genome. This method is useful for creating a transiently transgenic
CC plant where a heterologous transgene temporarily conveys a desired
CC phenotypic trait to the plant. Complete or nearly complete removal
CC of the heterologous DNA reduces the possibility of uncontrolled propagation
CC of the transgenic species and permits crops produced from the transgenic
CC plants to be co-mingled with non-transgenic crops for marketing
CC purposes. The method is useful for producing non-transgenic food
CC products from transgenic plants. The excision of the transgene occurs
CC only after the transgenic functions are either no longer needed, or the
CC continued presence of transgenes could cause concern. If transgenes are
CC excised from the host genome in response to a stimulus several days
CC prior to harvesting or marketing, potential negative effects of the
CC transgenes are reduced or eliminated. The progeny of the plants are also
CC essentially free of the transgene sequences. The method helps to reduce
CC potential health implications of transgenic food, to eliminate
CC undesirable spread of transgenes to the environment because pollen and
CC seeds produced from transgenic plants are non-transgenic, and to
CC protect proprietary rights inherent in the transgenic technology.
CC The present sequence represents the bacteriophage P1 Cre site specific
CC recombinase gene sequence, this sequence recognises the LoxP sequence.
CC The Cre/Lox site specific recombinase system may be used in the method
CC of the invention to excise heterologous DNA from a plant.
XX
SQ Sequence 1553 BP; 424 A; 340 C; 394 G; 395 T; 0 other;

Query Match 58.9%; Score 618.4; DB 24; Length 1553;
Best Local Similarity 74.8%; Pred. No. 3.1e-82;
Matches 775; Conservative 0; Mismatches 261; Indels 0; Gaps 0;

QY 14 AGAGGAGGTGAGCAACTGCTGACCGTGCACACGACCTGCCCGCCCTGCCCGTGAACG 73
Db 477 AGTGTAAATGTCCAAATTTACTGACCGTACACCAAAATTTGCCCTGCATTACCGGTCGATG 536
QY 74 CCACGACGAGGTGCGCAAGAACCTGATGGACATGTTCCGCGACCGCCAGCCCTTCA 133
Db 537 CAACGATGATGAGTTTCGCAAGAACCTGATGGACATGTTACGGGATCGCCAGCGGTTT 596
QY 134 GCGAGCACACCTGGAGATGCTGCTGAGCGTGTGCCCGCAGCTGCCCGCTGTGTGCAAGC 193
Db 597 CTGAGCATACCTGGAAAATGCTTCTGTCGGTTTCCCGGTCGTGGCGCGCATGGTCAAGT 656
QY 194 TGAACACCGCAAGTGTGTTCCCGCCGAGCCCGAGGACGTGGCGGCACTACCTGCTGTACC 253

Db 657 TGAATAACCGAAATGTTTCCCGCAACCTGAAGATGTTCCGCAATATCTTCTATATC 716
QY 254 TGCAGGCCCGCGCCTGGCCGTGAAGACCATTCAGCAGACACCTGGGGCAGCTGAACATGC 313
Db 717 TTCAGGCGCGCGTCTGGCAGTAAAACTATTCAGCAACATTTGGGCCAGCTAAACATGC 776
QY 314 TGCACCGCCGACAGCGCTGCCCGCCCGCCAGCAGCAAGCGCGTGTGAGCTGTGTATGC 373
Db 777 TTTATCGTGGTCCGGCTGCCACGACCAAGTACAGCAATGTCTTTCATCTGTTATGC 836
QY 374 GCGCATCCGCAAGGAGACGTGAGCGCGCGAGCGCGCAAGCAGCGCCCTGGCCTTCG 433
Db 837 GCGGATCCGAAAGAAACGTTGATGCCGTTGAACGTGCAAAACAGGCTCTAGCGTTCG 896
QY 434 AGCGCACCGACTTTCGACCGAGTGCAGCGCTGTGAGAAACAGCAGCCGCTGCCAGACA 493
Db 897 AACGCATGATTTGACCGAGTTCGTTCACTCATGGAANAATAGCGATCGCTGCAGGATA 956
QY 494 TCCGCAACCTGGCCTTCTGGGGCATCGCTTACAAACCTCTGTGTGCGCATCGCCGAGATCG 553
Db 957 TACGTAATCTGGCATTTCTGGGGATTCCTTATAACACCTCTGTACGTATAGCCGAAATG 1016
QY 554 CCCGCATCCGCGTGAAGGACATCAGCGGACCGACCGCGCCGCTGCTGATCCACATCG 613
Db 1017 CCAGGATCAGGGTTAAAGATATCTCAGTACTCAGCGTGGGAGAATGTTAATCCATATG 1076
QY 614 GCGCCACCAAGACCTTGTGAGCACCGCGCGCTGGAGAGGCGCTGAGCCTGGGGCTGA 673
Db 1077 GCAGAACGAAACGCTGTTAGCACCGCAGGTGTAGAGAGGACACTTAGCTGGGGGTAA 1136
QY 674 CCAAGCTGTGGAGCGCTGTGATCAGCGTGTAGCGGCTGGCCGACGACCCCAACTTACC 733
Db 1137 CTAACCTGTGTCGAGCATGATTTCCGCTCTCTGCTGTAGCTGATGATCCGATAACTACC 1196
QY 734 TGTCTTCCGCGTCCGCAAGACGGGTGCGCGCCGCCCGCCAGCCGACCGACCTGAGCA 793
Db 1197 TGTCTTCCGCGTCCGCAAGACGGGTGCGCGCCGCCCGCCAGCCGACCGCTATCAA 1256
QY 794 CCCGCGCCTTGGAGGCGCATCTTCAGGCGCACCCACCGCTGATCTAGCGCGCAAGACG 853
Db 1257 CTGCGCCCTTGGAGGAGATTTTGAAGCAACTCATCGATTGATTACGGCGCTAAGATG 1316
QY 854 ACAGCGCCAGCGCTACCTGGCTGGAGCGGCCACAGCGCCGCGCGCGCCCGCGCG 913
Db 1317 ACTCTGCTCAGAGATACCTGGCTGCTGGAACAGTGCCTGCTGCGAGCGCGCGAG 1376
QY 914 ACATGGCCGCGCGCGGTGAGCATCCCGAGATCATGAGCGCGCGCGGTGACCAACG 973
Db 1377 ATATGGCCGCGCGGTGAGTTTCAATACCGAGATCATGCAAGCTGTGGCTGGACCAATG 1436
QY 974 TGAACATCGTGTGAATACTACATCCGCAACCTGGACAGCGAGACCGCGCGCATGCTGCGCC 1033
Db 1437 TAAATATTGTCATGAATACTATATCCGTAACTGTGATGTGAACAGGGGCAATGCTGCGCC 1496
QY 1034 TGCTGAGGACGGCGA 1049
Db 1497 TGCTGAGGATGGCGA 1512

Search completed: December 16, 2003, 01:47:41
Job time : 370 secs

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OM nucleic - nucleic search, using sw model

Run on: December 16, 2003, 01:32:08 ; Search time 86 Seconds

(without alignments)
5388.980 Million cell updates/sec

Title: US-09-662-128A-1

Perfect score: 1050

Sequence: 1 atgcccaagaagaaggaa.....gcctgtgaggagcgcgac 1050

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*

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3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*

4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*

5: /cgn2_6/ptodata/2/ina/PTUS COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	755	71.9	2346	3	US-09-193-503B-5
2	755	71.9	2346	4	US-09-415-839-5
3	754.4	71.8	1032	3	US-09-193-503B-2
4	754.4	71.8	1032	4	US-09-415-839-2
5	630	60.0	5261	4	US-09-770-315-7
6	617.4	58.8	1740	2	US-08-864-224-10
7	617.4	58.8	2346	3	US-09-193-503B-4
8	617.4	58.8	2346	3	US-09-193-503B-7
9	617.4	58.8	2346	3	US-09-193-503B-8
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12	617.4	58.8	2346	4	US-09-415-839-8
13	616.6	58.7	4491	4	US-08-837-863-23
14	241.2	23.0	699	2	US-08-735-609-11
15	241.2	23.0	699	2	US-08-735-609-11
16	241.2	23.0	699	3	US-09-315-372-11
17	241.2	23.0	699	3	US-09-244-752-11
18	241.2	23.0	699	3	US-09-245-497-11
19	241.2	23.0	699	4	US-09-562-919-11
20	88.6	8.4	2163	4	US-09-252-991A-5310
21	88.6	8.4	3282	4	US-09-252-991A-5256
22	88.6	8.4	4158	4	US-09-252-991A-5348
23	88.6	8.4	4953	4	US-09-252-991A-5227
24	88.2	8.4	3624	1	US-07-951-715A-6
25	88.2	8.4	3624	2	US-08-459-448A-6
26	88.2	8.4	3624	3	US-08-459-595A-6
27	88.2	8.4	3624	3	US-08-459-504B-6

28 88.2 8.4 3624 3 US-08-459-444-6 Sequence 6, Appli

29 88.2 8.4 3624 3 US-09-053-549-7 Sequence 7, Appli

30 88.2 8.4 3624 4 US-09-547-422-6 Sequence 6, Appli

31 87.6 8.3 3222 4 US-09-543-084A-29 Sequence 29, Appli

32 86.6 8.2 3468 1 US-07-951-715A-2 Sequence 2, Appli

33 86.6 8.2 3468 3 US-08-459-448A-2 Sequence 2, Appli

34 86.6 8.2 3468 3 US-08-459-595A-2 Sequence 2, Appli

35 86.6 8.2 3468 3 US-08-459-504B-2 Sequence 2, Appli

36 86.6 8.2 3468 3 US-08-459-444-2 Sequence 2, Appli

37 86.6 8.2 3468 3 US-09-053-549-3 Sequence 2, Appli

38 86.6 8.2 3468 4 US-09-547-422-2 Sequence 7, Appli

39 86 8.2 4039 4 US-09-205-448-7 Sequence 26, Appli

40 86 8.2 4050 4 US-09-543-084A-26 Sequence 28, Appli

41 86 8.2 4093 4 US-09-543-084A-28 Sequence 4, Appli

42 85.6 8.2 975 3 US-09-365-150-4 Sequence 76, Appli

43 85.4 8.1 4767 4 US-09-231-899-76 Sequence 26, Appli

44 85.2 8.1 1965 3 US-09-178-252-26 Sequence 31, Appli

45 84.4 8.0 2929 4 US-09-543-084A-31

ALIGNMENTS

RESULT 1

US-09-193-503B-5

; Sequence 5, Application US/09193503B

; Patent No. 6262341

; GENERAL INFORMATION:

; APPLICANT: Baszczynski, Christopher L.

; APPLICANT: Lyznik, Leszek A.

; APPLICANT: Gordon-Kamm, William J.

; APPLICANT: Guan, Xueni

; APPLICANT: Rao, Guru

; APPLICANT: Tagliani, Laura A.

; TITLE OF INVENTION: A No. 6262341el Method For The Integration Of Foreign DNA Into

; FILE REFERENCE: 5718-66 (amended listing)

; CURRENT APPLICATION NUMBER: US/09/193,503B

; CURRENT FILING DATE: 1998-11-17

; PRIOR APPLICATION NUMBER: 60/099,435

; PRIOR FILING DATE: 1998-09-08

; PRIOR APPLICATION NUMBER: 60/056,627

; PRIOR FILING DATE: 1997-11-18

; PRIOR APPLICATION NUMBER: 60/065,613

; PRIOR FILING DATE: 1997-11-18

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 2346

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: sequence

; OTHER INFORMATION: encoding moCre:FLPm, Cre from Bacteriophage p1 and

; OTHER INFORMATION: FLP from Saccharomyces, both maize preferred

; OTHER INFORMATION: Codons

; NAME/KEY: CDS

; LOCATION: (1)..(2346)

US-09-193-503B-5

Query Match 71.9%; Score 755; DB 3; Length 2346;

Best Local Similarity 83.4%; Pred. No. 2.8e-120; Indels 0; Gaps 0;

Matches 857; Conservative 0; Mismatches 170;

Qy 23 TGAGCAACCTGCTGACGTCACAGAACCTGCGCCCTGCGCGTGGAGCCGACCG 82

Db 2 TGTCACCTGCTCAGGTTTCCAGAACCTTCGGCTCTTCCAGTGGAGCGCGTCG 61

Qy 83 ACAGGTGCGCAGAACCTGATGACATGTCGCGACCGCCAGGCTTCAGCGAGCACA 142

Db 62 ATGAAGTCAGGAGAACCTCATGACATGTTCCGCGACAGGCAAGCTTCAGCGAGCACA 121

Qy 143 CCTTGAAGATGCTGCTGAGCGTGTGCGGAGCTGGGCGCGCTGGTGCAGTGAACACC 202


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Qy 124 CAGCCCTTACGAGACACACTGGAAGATGCTGTAGCGTGTGCGCAGACTGCGCGCC 183
Db 1321 CAGCGCTTCTGAGCATACCTGGAATACTGTTCTGTCCGTTTCCCGTGTGCGCGGCA 1380
Qy 184 TGGTGAAGCTGACACACCGCAAGTGTTCCTCCCGCAGCCGAGCGACGTGCGGACTAC 243
Db 1381 TGGTGAAGTTGAATAACCGGAATGTTTCCCGCAGAACCTGAAGATGTTCGCGATTAT 1440
Qy 244 CTGCTGTACCTCGAGCGCCGCGCTGCGCTGAGACCATCAAGCAGCACCTGGGCGAG 303
Db 1441 CTTCTATATCTTACGGCGCGGCTGCGCAGTAATAAATACTATCAGCAACATTTGGGCGAG 1500
Qy 304 CTGAACATGTCACCCCGCAGCGGCTGTGCCCCCGCCAGCAGCAGCAACCGGTGAGC 363
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Qy 364 CTGCTGATGCGCGCATCCGACAGGAGAACTGACGCGCGGAGCGCGGCGCAAGCGGC 423
Db 1561 CTGCTGATGCGGCGGATCCGAAAAGAAAACGTTGATCCCGTGAACGTGCAAAACAGGCT 1620
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Db 1681 TGCAGGATATACGTAATCTGGCAATTTCTGGGGATTCGTTATAACCCCTGTTACGTATA 1740
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Qy 604 ATCCACATCCGCGCACCAAGACCTCTGTGAGCACCGCGCGGTGGAGAGGCGCCTGAGC 663
Db 1801 ATCCATATTCGAGAACGAAACGCTGTTAGCACCGCAGGTGTAGAGAGGCACTTAGC 1860
Qy 664 CTGGCGTGTACCAAGCTGTGGAGCGCTGTGATCAGCGTGTAGCGCGTGGCGGACGACCCC 723
Db 1861 CTGGGGTAACTAACTGGTCGAGCGATGGATTTCCGCTCTCTGTGTGTAGCTGATCGC 1920
Qy 724 AACNACTACTGTTCTCGCGTCCGCAAGAACGCGTGGCGCGCCCGCAGCGCCACGAC 783
Db 1921 AATAACTACTGTTTTCGCGGTTCAGAAAAAATGTTGTCGCGCGCATCTGCGCACGAC 1980
Qy 784 CAGCTGAGCACCCGCGCCCTGGAGGCGATCTTCAGGCGCACCCACCGCCTGATCTACGGC 843
Db 1981 CAGTATCACTCGCGCCCTGGAAGGATTTTGAAGCACTCATCGATTGATTACGGC 2040
Qy 844 GCCAAGACGACAGCGCCAGCGCTACTGCGCCTGGAGCGGCCACAGCGCCCGCGTGGC 903
Db 2041 GCTAAGGATGACTCTGTGTACAGATACTGCGCCTGGTCTGACACAGTGGCCGTTGCGGA 2100
Qy 904 GCGCCCGCGACATGCGCGCGCGCGTGTAGCATCTCCCGAGATCATGACGCGCGCGGC 963
Db 2101 GCGCGCGAGATATGGCGCGCGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGGTGGC 2160
Qy 964 TGGACCAAGTGAACATCTGATGAACCTACATCCGCAACCTGGACGAGACCGCGCGCC 1023
Db 2161 TGGACCAATGTAATATTTGTCATGAACTATATCCGTAACCTGGATATGTGAACAGGGGCA 2220
Qy 1024 ATGTTGCGCCTGTGAGGAGCGGCA 1049
Db 2221 ATGTTGCGCCTGTGGAAGATGGCGA 2246
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RESULT 6

US-08-864-224-10

; Sequence 10, Application US/08864224

; Patent No. 5851808

; GENERAL INFORMATION:

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; APPLICANT: Ellledge, Stephen J.
; APPLICANT: Liu, Qinghua
; TITLE OF INVENTION: Rapid Subcloning Using Site-Specific
; TITLE OF INVENTION: Recombination
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/864,224
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: BCM-02681
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1740 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1737
; US-08-864-224-10
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Query Match 58.8%; Score 617.4; DB 2; Length 1740;
Best Local Similarity 75.1%; Pred. No. 6.1e-97;
Matches 771; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

Qy 23 TGAGCAACCTGTGACCGTGCACAGAACTGCCCGCCCTGCCGTGGAGCGCCACCGCG 82
Db 710 TGGCCAATTTACTGACCGTACACCAAAATTTGCTGCAATTACCGGTGATGCAACGAGTG 769
Qy 83 ACAGGTGCGCAGAAGACCTGATGGACATGTTCCGCGACCGCCAGGCTTCAGCGAGCACA 142
Db 770 ATGAGGTTCGCAAGAACCTGATGGACATGTTTCAGGGATCGCCAGGCGTTTCTTGAGCATA 829
Qy 143 CCTGGAAGATGCTGCTGAGCGTGTGCGCAGCTGGGCGCGCTGCTGCAAGCTGAACAACC 202
Db 830 CCTGGAAGATGCTTCTGTGCGTTTGGCGGCGCATGCTGCAAGTTGAATACC 889
Qy 203 GCAAGTGGTTCCCGCGGAGCCCGAGGACGTGCGCGACTACCTGCTGTACTCAGGCGCC 262
Db 890 GGAATGGTTTCCCGCAGAACCTGAAGATGTTCCGCGATTATCTTCTATATCTTTCAGSGCG 949
Qy 263 GCGCGCTGCGCGTGAAGACCATCCAGGACCATCTGGGCGAGCTGAACATGCTGCGACCGCC 322
Db 950 GCGGTCCTGGCAGTAAAAACTATCCAGCAACATTTGGGCCAGCTAAAAACATGCTTCATCGTC 1009
Qy 323 GCAGCGCGCTGCCCGCCCGCAGGACGAGCAACCGCTGAGCGCTGGTGTGCGCGCATCC 382
Db 1010 GGTCCGCGCTGCCCGCAGCAACGAGTGAAGCAATGCTGTTTCACTGGTTATGCGGCGGATCC 1069
Qy 383 GCAAGGAGACGTGGACGCGCGGAGCGCGCCAGCAGGCGCTTGGCGCTTCGAGCGCACCG 442
Db 1070 GAAAGAAAACGTTGATCGCGGTGAACGTGCAAAACAGGCTCTAGGCTTCGAGCGCACTG 1129
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QY 443 ACTTCGACGAGTGCAGCGCTGATGAGAAAGCGACCGCTGCGCAGGACATCCGCAACC 502
Db 1130 ATTTCGACGAGTTCGTTCACTCATGGAATAAGCATGCTGCCAGGATATACGTAATC 1189
QY 503 TGGCCTTCCTGGGATCGCTCAACACACCTGCTGCGCATCGCGAGATCGCCGCGCATCC 562
Db 1190 TGGCATTTCTGGGGATTGCTTATAACACCTGTTAGTATAGCCGAAATTCGAGATCA 1249
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Db 1250 GGGTTAAGATATCTCACTGATGACGGTGGGAGATGTTAATCCATATTGGCAGAACGA 1309
QY 623 AGACCTGTGTGACACCGCGCGGTGAGAAAGCCCTGAGCCTGGCGGTGACCAAGTGG 682
Db 1310 AAACGCTGTGTAGCACCGCAGGTGTAGAGAAAGCACTTAGCCTGGGGTAACTAAACTGG 1369
QY 683 TGGAGCGCTGGATCAGCGTGAGCGGTGGCGGACGACGCCCAACAACTACTCTGTTGCC 742
Db 1370 TCAGAGCATGGATTTCGCTCTCTGGTGTAGTGTATCCGAAATATCACTCTGTTGCC 1429
QY 743 GCGTGGCGAAGAACGGCGTGGCGCGCCCGCCAGCGCCACACCGCTGAGCACCCGGGCC 802
Db 1430 GCGTCAGAAATAATGGTGTGGCGGCCATCTGCCACCGCAGCTATCAACTCGCGGCC 1489
QY 803 TGGAGGCACTTCGAGGCCACCCACCGCCTGATCTACGGGCGCAAGGACGACGCGCC 862
Db 1490 TGAAGGGATTTTGAAGCAACTCATCGATTGATTATACGGCGCTAAGGATGACTCTGGTC 1549
QY 863 AGCGTACCTGGCTGAGCGGCCACAGCGCCCGCGTGGCGCGCGCGGACATGGCCC 922
Db 1550 AGATATACCTGGCTGTCTGGACACAGTGCCTGTGCGAGCGCGCGAGATATGGCCC 1609
QY 923 GCGCGCGGTGAGCATCCCGAGATCATGAGCGCGCGGTGAGCAACCGTGAACATCG 982
Db 1610 GCGCTGAGTTTCAATACCGGAGATCATGCAAGCTGGTGGTGGACCAATGTAATATTG 1669
QY 983 TGATGAATACATCCGCAACTGACACGCGAGACCGCGCGCATGGTGGCGCTGCTGAGG 1042
Db 1670 TCATGAATATATCCGTAACTGGATAGTGAACAGGGGCAATGGTGGCGCTGCTGGAAG 1729
QY 1043 ACGCGCA 1049
Db 1730 ATGGCGA 1736

RESULT 7
US-09-193-503B-4
; Sequence 4, Application US/09193503B
; Patent No. 6262341
; GENERAL INFORMATION:
; APPLICANT: Baszczyński, Christopher L.
; APPLICANT: Lyznik, Leszek A.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Guan, Xueni
; APPLICANT: Rao, Guru
; APPLICANT: Tagliani, Laura A.
; TITLE OF INVENTION: A No. 6262341el Method For The Integration Of Foreign DNA Into
; TITLE OF INVENTION: Eukaryotic Genomes
; FILE REFERENCE: 5718-66 (amended listing)
; CURRENT APPLICATION NUMBER: US/09/193,503B
; CURRENT FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Nucleotide
; OTHER INFORMATION: sequence encoding a Cre:FLPm polypeptide, Cre
; OTHER INFORMATION: from Bacteriophage P1 and FLP (Maize preferred
; OTHER INFORMATION: codons) from Saccharomyces
US-09-193-503B-4
Query Match 58.8%; Score 617.4; DB 3; Length 2346;
Best Local Similarity 75.1%; Pred. No. 6.2e-97;
Matches 771; Conservative 0; Mismatches 256; Indels 0; Gaps 0;
QY 23 TGAGCAACCTGCTGACCGTGCACACGAACTCCCGCGCCCTGCGCGTGAACGCGCACAGCG 82
Db 2 TGGCAATTTACTGACCGGTACACCAAAATTTGCTTCATTCGCGTGCATGCAACGAGTG 61
QY 83 ACAGGTGCGCAAGAACCTGTATGAGCATGTTCCGCGACCCGCGAGCCTTCAGCGAGCA 142
Db 62 ATGAGGTTCCCAAGAACCTGTATGAGCATGTTCCAGGATCGCCAGCGGTTTCTGAGCATA 121
QY 143 CTGAGAGATGCTGCTGAGCGGTGCGCGAGCTGGCGCGCTGCTGCAAGCTGCAACACC 202
Db 122 CTGGAATAATGCTTCTGCTCGGTTGCGCGTCTGGCGGCACTGGTCAAGTTGAATAACC 181
QY 203 GCAAGTGGTTCCCGCGGAGCGCGAGACGTGCGGACTACCTGTGTACTCTGACGCGCC 262
Db 182 GGAATGTTTCCCGAGAACCTGAGATGTTTCGCAATTATCTTATATCTTCAGCGCG 241
QY 263 GCGCCTGCGCGTGAAGAACCTATCCAGACACCTGGGCCAGTGAACATGCTGCACCGCC 322
Db 242 GCGGTCTGCGAGTAAACATATCCAGCAACATTTGGCGCAGCTAAACATGCTTCATCGTC 301
QY 323 GCAGCGCTGCGCGCCCGCGCGAGCAGCAAGCCGCTGAGCTGGTGTGATGCGCGCATCC 382
Db 302 GGTTCGCGGTGCGCACCAAGAGTGACAGCAATGCTGTTTCACTGGTATGCGCGGATCC 361
QY 383 GCAAGGAGAACGTGGACGCGCGAGCGCGCCAGCAGCGCCCTGGCGCTTCGAGCGCACCG 442
Db 362 GAAAGAAACGTTGATGCGGTGAACCTGCAAAACAGGCTTAGCGTTTGAACGCACTG 421
QY 443 ACTTCGACGAGTGCAGCCTGATGAGAAACAGCGCCGCTGCGAGGACATCCGCAACC 502
Db 422 ATTTGACACGAGTTCTGTTCACTCATGGAATAAGCATGCTGCCAGGATATACGTAATC 481
QY 503 TGGCCTTCCTGGGATCGCTCAACACCTGCTGCGCATCGCGGAGATCGCCGCGCATCC 562
Db 482 TGGCATTTCTGGGGATTGCTTATAACACCTGTTACCTATAGCCGAAATTCGCGAGATCA 541
QY 563 GCGTGAAGGACATCAGCGCGCACCGCGCGCGCATGCTGATCCACATCGCGCGCACCA 622
Db 542 GGGTTAAGATATCTCACTGATGAGCGTGGGAGATGTTAATCCATATTGGCAGAACGA 601
QY 623 AGACCTGTGTGACACCGCGCGGTGAGAAAGCCCTGAGCCTGGCGGTGACCAAGTGG 682
Db 602 AAACGCTGTGTAGCACCGCAGGTGTAGAGAAAGCACTTAGCCTGGGGTAACTAAACTGG 661
QY 683 TGGAGCGCTGGATCAGGTGAGCGGTGCGCGACGACCCCAACAACTACTCTGCTGCC 742
Db 662 TCGAGCGATGGATTTCCGCTCTGCTGTTAGTATGATCGGAATAACTACTCTGTTTGGC 721
QY 743 GCGTGGCGAAGAACGGCGTGGCGCGCCCGCGCGCATCGCGCAGCTGAGCACCCGGGCC 802
Db 722 GGGTCAGAAAAATGTTGTTGCGCGCCATCTGCCACGACGAGCTATCACTTCGCGCCC 781
QY 803 TGGAGGCACTTTTCGAGGCCACCCACCGCTGATCTACGGCGCAAGGACGACAGCGGCC 862
Db 782 TGAAGGGATTTTGAAGCAACTCATCGATTGATTTACGGCGCTAAGGATGACTCTGCTC 841
QY 863 AGCGTACCTGCGCTGAGCGCGCACAGCGCGCGCTGGCGCGCGCGCGCATGCGCCC 922
Db 842 AGAGATACCTGGCTGTGGACACAGTGCCTGTCGAGCGCGCGCGAGATATGGCCC 901
QY 923 GCGCGCGGTGAGCATCCCGAGATCATGCGAGCGCGCGCGCTGACCAACGTAACATCG 982

Db 902 GCCTGGAGTTTCAATACCGAGATCATGCAAGCTGGTGGCTGGACCAATGTAATATTG 961
QY 983 TGATGAACATACCTCCGCAACTGGACAGCGAGACCGCGCATGTGCGCTGCTGGAGG 1042
Db 962 TCATGAACATATACCGTAACCTGGATAGTGAACACAGGGCAATGGTGGCTGCTGGAAG 1021
QY 1043 ACGGCGA 1049
Db 1022 ATGGCGA 1028

RESULT 8
US-09-193-503B-7
; Sequence 7, Application US/09193503B
; Patent No. 6262341
; GENERAL INFORMATION:
; APPLICANT: Baszczynski, Christopher L.
; APPLICANT: Lyznik, Leszek A.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Guan, Xueni
; APPLICANT: Rao, Guru
; APPLICANT: Tagliani, Laura A.
; TITLE OF INVENTION: A No. 6262341el Method For The Integration Of Foreign DNA Into
; FILE REFERENCE: 5718-66 (amended listing)
; CURRENT APPLICATION NUMBER: US/09193,503B
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence
; OTHER INFORMATION: encoding a Cre:FLP polypeptide, Cre from
; OTHER INFORMATION: Bacteriophage P1 and FLP from Saccharomyces
US-09-193-503B-7

Query Match 58.8%; Score 617.4; DB 3; Length 2346;
Best Local Similarity 75.1%; Pred. No. 6.2e-97;
Matches 771; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

QY 23 TGAGCAACCTGCTGACCGTGACCGAGAACCTGCGCCGCTGCGGAGCGCCACCGAGCG 82
Db 2 TGCCCAATTTACTGACCGTGACCAAAATTTGCTGATTAACCGTGCATGCAACGAGTG 61
QY 83 ACGAGTGCGCAGAACCTGATGACATGTTCCGCGACCGCGGCTTCAGGAGGACACA 142
Db 62 ATGAGGTTCCGAAGAACCTGATGACATGTTCCAGGATCGCAGCGGCTTTCTGAGCATA 121
QY 143 CCTGGAGATGCTGCTGAGCGTGTCGCGAGCTGGCGGCGCTGGTGAAGCTGAACAAC 202
Db 122 CCTGGAAATGCTTCTGCTGCTTTCGCGGCTGCTGGCGGCGATGGTGAAGTTGAATAAC 181
QY 203 GCAAGTGGTTCCCGCGGAGCCCGAGGACGTGCGGACTACCTGCTGCTACTGCGAGGCC 262
Db 182 GGAATGGTTCCCGCAGACCTGAAGATGTTCCGGAATATCTCTATATCTTCAGGCGC 241
QY 263 GCGGCTGGCGGTGAAGACCATCAGCAGACCTGGCCAGCTGAACATGCTGCAACGCC 322
Db 242 GCGGCTGGCAGTAAATACTATCAGCAACATTTGGCCAGCTAAACATGCTTCATCGTC 301
QY 323 GCAGCGGCTGCGCGCGCCCGCAGCAGCAGCAGCAGCGCTGGTGGTATGCGCGCATCC 382
Db 302 GGTCCGGGCTGCCACGACCAAGTGACAGCAATGCTGTTTCACTGGTTATGCGCGGATCC 361

QY 383 GCAAGGAGAACGTGGACCGCGGAGCGGCCAAGAGGCGCTTGGCTTTCGAGCGCACCG 442
Db 362 GAAAGAGAAACGTTGATCGCGTGAACCGTGCAAAAACAGGCTTAGCGTTTGAACGCACTG 421
QY 443 ACTTCGACAGGTGCGCAGCTGATGAGAAACAGAGACCGCTGCCAGAGACATCCGCAACC 502
Db 422 ATTTGACACAGGTGCTTCACTCATGGAATAAGGATCGCTGCCAGGATATACGTAATC 481
QY 503 TGGCCTTCTGGGATCGCCTACAACACCTCTGCGCATCGCGAGATCGCCCGCATCC 562
Db 482 TGGCATTTCTGGGATTCCTTATAACACCTCTTACGTATAGCCGAAATTCGCGATCA 541
QY 563 GCGTGAAGACATCAGCCGACCGAGCGCGCGCATGCTGATGCATCGCGCGGACCA 622
Db 542 GGGTTAAAGATATCTCACGTACTGACGGTGGGAGAATGTTAATCATATATTCAGAACGA 601
QY 623 AGACCTGCTGAGACCGCGCGCTGGAGAGGCGCTGAGCGCTGGGCGTGACCAAGCTGG 682
Db 602 AAACGCTGTTAGCACCGCAGGTGAGAGAGGCACTTAGCCTGGGGTAACTAACTGG 661
QY 683 TGGAGCGCTGATCAGCGCTGAGCGCGTGGCGGAGACCGCCCAACAACTACCTGTTCTGCC 742
Db 662 TCGAGCGATGGATTTCCGCTCTCTGTTGATGATGATCCGAATACTACCTGTTTGGC 721
QY 743 GCGTGGCAGAAACGCGCTGGCGGCCCGCAGCGCCACAGCGCAGCTGAGCACCAGCGGCC 802
Db 722 GGGTCAGAAAAAATGGTGTTCGCGGCGCATCTGCCACAGCAGCTATCAACTCGCGGCC 781
QY 803 TGGAGGCGATCTTCGAGGCGCACCGCTGATCTACCGCGCGCGCGCGCGCATCGGCC 862
Db 782 TGAAGGGATTTTGAAGCAACTCATCGATGATTACCGCGCTAAGGATGACTCTGGTC 841
QY 863 AGCGCTTACCTGCGCTGGAGCGCCACAGCGCGCGCGCGCGCGCGCGCATCGGCC 922
Db 842 AGAGATACCTGCGCTGCTGGACACAGTGCCCGTGTGCGAGCGCGCGGATATGCGCC 901
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Db 902 GCGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGGTGGCTGGACCAATGTAATATTG 961
QY 983 TGATGAACATACCTCCGCAACCTGGACAGCGAGACCGCGCGCGCGCTGCTGCGCTGCTGAGG 1042
Db 962 TCATGAACATATATTCGTAACCTGGATAGTGAACACAGGGGCAATGGTGGCGCTGCTGGAAG 1021
QY 1043 ACGGCGA 1049
Db 1022 ATGGCGA 1028

RESULT 9
US-09-193-503B-8
; Sequence 8, Application US/09193503B
; Patent No. 6262341
; GENERAL INFORMATION:
; APPLICANT: Baszczynski, Christopher L.
; APPLICANT: Lyznik, Leszek A.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Guan, Xueni
; APPLICANT: Rao, Guru
; APPLICANT: Tagliani, Laura A.
; TITLE OF INVENTION: A No. 6262341el Method For The Integration Of Foreign DNA Into
; FILE REFERENCE: 5718-66 (amended listing)
; CURRENT APPLICATION NUMBER: US/09193,503B
; CURRENT FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 8
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence
; OTHER INFORMATION: encoding a FLPm:Cre polypeptide, FLP from
; OTHER INFORMATION: Saccharomyces (maize preferred codons), and Cre
; OTHER INFORMATION: from Bacteriophage P1
; NAME/KEY: CDS
; LOCATION: (1)..(2346)
US-09-193-503B-8

Query Match      58.8%; Score 617.4; DB 3; Length 2346;
Best Local Similarity 75.1%; Pred. No. 6.2e-97;
Matches 771; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

QY 23 TGAGCAACCTGCTGACCGTGCACAGACCTGCCCGCCCTGCCCGTGCAGCGCCACACGCG 82
Db 1316 TGGCCAATTACTGACCGTGCACCAAAATTTGCTGCATTAACCGTGCATGCAAGAGTG 1375

QY 83 ACAGAGTGCAGCAAGCACTGATGACATGTTCCGCGACCGCCAGCGCTTCAGCGAGCACA 142
Db 1376 ATGAGGTTCGACAGCACTGATGACATGTTTCAGGATCGCCAGCGCTTTCTGAGCATA 1435

QY 143 CTTGGAAGATGCTGCTGAGCGTGTGCGCGAGCTGGCGCGCTGTGTGCAAGCTGAAACAAC 202
Db 1436 CTTGGAAGATGCTGCTGCGGTTTTCGCGGTGCTGGCGGCGATGTTGCAAGTTGAATAAC 1495

QY 203 GCAAGTGGTTCCTCCGCGAGCCGAGGAGCGCGCACTACTCTGCTGTAACCTGAGCGCC 262
Db 1496 GGAATGGTTCCTCCGCGAGACTGAAGATGTTCCGATATCTCTATATCTTCAGCGCG 1555

QY 263 GCGGCTGGCGGTGAGAACCACTCCAGCAGCACTGGGCGACCTGGAACATGCTGCACGCC 322
Db 1556 GCGCTCTGGCAGTAAACTATCCAGCAACATTTGGGCGAGCTAAACATGCTTCACTGTC 1615

QY 323 GCAGCGCTGCTCCCGCCCGCCAGCAGCAAGCGCTGAGCTGTGTGATGCGCGCATCC 382
Db 1616 GGTCCGGCTGCCAGCAAGTGCACAAATGCTGTTTCACTGTTATGCGCGGATCC 1675

QY 383 GCAAGGAGAGCTGGAGCGCGCGAGCGCGCAGCAGCGCTGCTGCTGAGCGCAACCG 442
Db 1676 GAAAGGAGAGAGCTGATGCCCGTGAACGCTGCAAGAGCTGCTAGCGTTGCAAGCACTG 1735

QY 443 ACTTCGACAGGTGCGCAGCTGTATGGAGAACAGCAGCGCTGCCAGGACATCCGCAAC 502
Db 1736 ATTTGACAGGTTCGTTCACTCATGGAAATAGCATGCTGCCAGGATATACGTAATC 1795

QY 503 TGGCCTTCTGGGATCGCCCTAACAACCCCTGCTGCGCATCGCGAGTCCGCGCATCC 562
Db 1796 TGGCATTTCTGGGGATTGCTTATAACACCCTGTTACGTATAGCCGAAATGCCAGGATCA 1855

QY 563 GCGTGAAGGACATAGCGCGCACCGAGCGCGCGCTGCTGATCCACATCGCGCGCACCA 622
Db 1856 GGGTTAAGATATCTCAGTACTGACGTGGAGAGATGTTATCCATATTGGCAGACGA 1915

QY 623 AGACCTTGATGAGCACCAGCGCTGAGAGAGCGCTGAGCGCTGGCGGTGACCAAGCTGG 682
Db 1916 AAACCTTGATGAGCACCAGCTGATGAGAGAGCACTTAGCTGGGGTAACTAACTAGT 1975

QY 683 TGGAGCGTGGATAGCGGTGAGCGGTGGCGGAGCGACCCCGAACAACTACCTGTTCTGCC 742
Db 1976 TCGAGCGATGGAATTTCCGTTCTGCTGTAGCTGATGATCCGAAATAACTACCTGTTTTC 2035

QY 743 GGGTGGCAAGAACCGCTGGCGCCCGCCAGCGCCAGCGAGCTGAGCAACCGCGGCC 802
Db 2036 GGGTCAGAAAAATGGTGTGCGCGCCATCTGCGCCAGCGAGCTATCACTCCCGGCC 2095

QY 803 TGGAGGGCATCTTCAGGAGCCACCCACCGCTGATCTACGGCGCCAGGACGACAGCGCC 862
Db 2096 TGGAGGGATTTTGAAGCAACTCATCGATTGATTATACGGGCTAAGGATGACTCTGGTC 2155

; SEQ ID NO 863
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Nucleotide
; OTHER INFORMATION: sequence encoding a Cre,FLPm polypeptide, Cre
; OTHER INFORMATION: from Bacteriophage P1 and FLP (Maize preferred
; OTHER INFORMATION: codons) from Saccharomyces
US-09-415-839-4

Query Match      58.8%; Score 617.4; DB 4; Length 2346;
Best Local Similarity 75.1%; Pred. No. 6.2e-97;
Matches 771; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

QY 23 TGAGCAACCTGCTGACCGTGCACAGAACCTGCCCGCCCTGCCCGTGCAGCGCCACACGCG 82
Db 2 TGGCCAATTACTGACCGTGCACCAAAATTTGCTGCATTAACCGTGCATGCAAGAGTG 61

QY 83 ACAGAGTGCAGCAAGCACTGATGACATGTTCCGCGACCGCGAGCGCTTCAGCGAGCACA 142
Db 62 ATGAGGTTCGACAGCACTGATGACATGTTTCAGGATCGCCAGCGCTTTCTGAGCATA 121

QY 143 CTTGGAAGATGCTGCTGAGCGTGTGCGCGAGCTGGCGCGCTGTGTGCAAGCTGAAACAAC 202
Db 122 CTTGGAAGATGCTGCTGCGGTTTTCGCGGTGCTGGCGGCGATGTTGCAAGTTGAATAAC 181

QY 203 GCAAGTGGTTCCTCCGCGAGCCCGAGGAGCGCTGCCGCACTACTCTGCTGTAACCTGAGCGCC 262
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182	DB	GGAAATGGTTTCCGCGAGAACTTGAGATGTTTCGGGATTAATCTTTATATCTTTCAGGCGC	241
263	QY	CGCGCCTGGCGGTGAAGAACCATCCAGCAGCACCTGGGCCAGCTGAAACATGCTGCACCGCC	322
242	DB	CGCGTCTGGCAGTAAAAAATATCCAGCAACATTTGGGCCAGCTAAAAACATGCTTCATCGTC	301
323	QY	GCAGCGCCTGCCCGGCCGAGCAGACAGCAACCGGTGAGCCTGTGATGCGCGCGCATCC	382
302	DB	GGTCCGGGCTGCCACGACCAAGTGACAGCAATGCTGTTTCACTGGTTATGCGCGGATCC	361
383	QY	GCAAGGAGAACGTTGGAGCCGCGGAGCGGCCCAAGCAGAGCCCTTGGCCTTCGAGCGCACCG	442
362	DB	GAAAGAAACGTTGATGCCGGTGAACTGCAAAACAGGCTCTAGCGTTTCGACGCGACTG	421
443	QY	ACTTTCGACAGGTCCGAGCGCTGATGAGAAACAGACCGCTGCGAGGACATCCGCAACC	502
422	DB	ATTTTCGACCAAGTTTCGTTCACTCATGAAAAATAGCGATCGCTGCCAGGATATACGTAATC	481
503	QY	TGGCCTTCTGGGCATCGCTTACAAACCTCTGCGCATCGCGAGATCGCCCGCATCC	562
482	DB	TGGCATTTCTGGGATTTGCTTTAACAACCCCTGTTACGTATAGCGAAATTCACGAGATCA	541
563	QY	CGCTGAAGGACATCAGCGCGCACCGACCGCGCGCATGCTGTATCCACATCGGCGGACCA	622
542	DB	GGGTTAAAGATATCTCACTACTACCGCTGGAGAAATGTTTAATCCATATTTGGCAGAACGA	601
623	QY	AGACCTCTGTGAGCACCGCGCGTGGAGAGGCCCTGAGCCTGGGGGTGACCAAGCTGG	682
602	DB	AAAACGCTGGTTAGCACCGCAGGTGTAGAGAGGCACCTTAGCCTGGGGGTAACTAATCTG	661
683	QY	TGGAGCGCTGGATCAGCGTGAAGCGCGTGGCGCGACGACCCCAACACTACTGTTCTTGCC	742
662	DB	TCGAGCGATGATTTCCGTCCTGCTGTAGCTGATGATCCGAATACTACTGTTTGTGCC	721
743	QY	CGCTGCGCAAGAAACGGCGTGGCGCGCCCGCCAGCGCAACGACGCTGAGCACCGGGCCC	802
722	DB	GGGTGAGAAAAATGGTTTCCCGCGCATCTGCGACGACGACGATCAACTCGCGCCC	781
803	QY	TGGAGGGCATCTTCGAGGCCACCCACCGCCTGATCTAGCGCGCCAGGACGACAGCGGCC	862
782	DB	TGGAAGGATTTTGAAGCAACTCATCGATTGATTTACGGCGCTTAAGAGTAGCTGTGTC	841
863	QY	AGCGTACTCTGGCTGGAGCGGCCACAGCGCCCGCTGGCGCGCCCGCCGACATGSCCC	922
842	DB	AGAGATACCTGGCCTGGTCTGGACACAGTGCCTGTCGGAGCGCGCGAGATATGSCCC	901
923	QY	GGCGCGCGTGAGCATCCCCGAGATCATGAGCGCGCGGCTGACCAACGTGACATCG	982
902	DB	CGCTTGGAGTTTCAATATCCGAGATCATGCAAGCTGTGGCTGGACCAATGTAATATTG	961
983	QY	TGATGAATACATCCGCAACCTGGACACGAGACCGCGCCCATGGTGGCGCTGCTGGAGG	1042
962	DB	TCATGAATATATCGTTAACTGATAGTAGAAACAGGGGCAATGTTGGCCTGCTGGAAG	1021
1043	QY	ACGGCGA	1049
1022	DB	ATGGCGA	1028

RESULT 11

US-09-415-839-7
 ; Sequence 7, Application US/09415839
 ; Patent No. 6541231
 ; GENERAL INFORMATION:
 ; APPLICANT: Baszczyński, Christopher L.
 ; APPLICANT: Lyznik, Leszek A.
 ; APPLICANT: Gordon-Kamm, William J.
 ; APPLICANT: Guan, Xueni
 ; APPLICANT: Rao, Guru
 ; APPLICANT: Tagliani, Laura A.
 ; TITLE OF INVENTION: A No. 6541231el Method For The Integration Of Foreign DNA
 ; TITLE OF INVENTION: Into
 ; TITLE OF INVENTION: Eukaryotic Genomes

Db 662 TCAGCGGATGGATTTCCTGCTCTCTGGTGTAGCTGATCCGAATAACTACCTGTTTGGCC 721
Qy 743 GCGTGCAGCAAGAACCGCTGGCGCCGCCAGCGCCACAGCGAGCTGAGCACCAGCGGCC 802
Db 722 GGGTCAGAAAAAATGGTGTGGCGGCCATCTGCCACAGCCAGCTATCAACTCGCGGCC 781
Qy 803 TGGAGGCACTCTGAGGCCACCCACCGCTGATCTAGCGGCCCAAGAGACAGACGGGCC 862
Db 782 TGGAAAGGGATTTTGAAGCAACTCATCGATTGATTACGGCGCTAAGGATGACTCTGGTC 841
Qy 863 AGCGCTACCTGGCTGGAGCGGCCACAGCGCCCGGGTGGCGGCCCGCCGACATGGGCC 922
Db 842 AGAGATACCTGGCGCTGGTCTGACACAGTGGCGGTGTCGGAGCGCGGAGATATGGGCC 901
Qy 923 GCGCGCGCTGAGCATCCCGGAGATCATCAGCGCGCGCGCTGGACCAACGTTGAACATG 982
Db 902 GCGCTGGAGTTTCAATACCGGAGATCATCAAGCTGGTGGCTGGACCAATGTAATATTG 961
Qy 983 TGTGAACTACATCCCACTGGACAGCGAGACCGCGCCATGGTGGCGCTGCTGGAGG 1042
Db 962 TCATGAACATATATCCGTAACCTGGATAGTGAACAGGGGCAATGGTGGCGCTGCTGGAG 1021
Qy 1043 ACGGCGA 1049
Db 1022 ATGGCGA 1028

RESULT 12
US-09-415-839-8
; Sequence 8, Application US/09415839
; Patent No. 6541231
; GENERAL INFORMATION:
; APPLICANT: Baszzyński, Christopher L.
; APPLICANT: Lyznik, Leszek A.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Guan, Xueni
; APPLICANT: Rao, Guru
; APPLICANT: Tagliani, Laura A.
; TITLE OF INVENTION: A No. 6541231 Method For The Integration Of Foreign DNA
; TITLE OF INVENTION: Into
; FILE REFERENCE: 5718-66 (amended listing)
; CURRENT APPLICATION NUMBER: US/09/415,839
; CURRENT FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: US/09/193,503
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence
; OTHER INFORMATION: encoding a FLP:Cre polypeptide, FLP from
; OTHER INFORMATION: Saccharomyces (maize preferred codons), and Cre
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2346)
US-09-415-839-8

Query Match 58.8%; Score 617.4; DB 4; Length 2346;
Best Local Similarity 75.1%; Pred. No. 6.2e-97;
Matches 771; Conservative 0; Mismatches 256; Indels 0; Gaps 0;
Qy 23 TGAGCAACCTGCTGACCGTGCACAGAACCTTGGCGGCCCTGCGGTGGACGCCACCGG 82

Db 1316 TGGCAATTTACTGACCGTACACCAAAATTTGCTGCTGATACCGGTGATGCAACAGAGTG 1375
Qy 83 ACGAGGTGCGCAAGAACTGATGACATGTTCCGCGACCGCGAGCCCTTACGCGAGACA 142
Db 1376 ATGAGGTTCGCAAGAACTGATGACATGTTTCAGGGATTCGCGAGCGCTTTCTGAGCATA 1435
Qy 143 CCTGGAAGATCTGCTGAGCGTGTCCGCACTGGCGCGCTGTGTGCAAGCTGAACAAACC 202
Db 1436 CTTGGAATACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1495
Qy 203 GCAAGTGTTCCTCCCGAGAGCCGAGGACGTGCGCGACTACTGCTGTGATCTGAGGCCC 262
Db 1496 GGAATGTTCCTCCCGAGAACCTCAAGATGTTTCGCGATTATCTCTATATCTTCAGGCGC 1555
Qy 263 GCGGCTTGGCGTGAAGCAATCCAGAGCACTTGGGCGAGCTGAACTGCTGACCGCC 322
Db 1556 GCGGCTTGGCGTGAAGCAATCCAGAGCACTTGGGCGAGCTGAACTGCTGATCTGCTC 1615
Qy 323 GCAGCGGCTTCCCGCGCCAGCGACAGCAACGCGTGTGAGCTGTGATGCGCGCATCC 382
Db 1616 GGTCCGGCTGCGACGACCAAGTACAGCAATGCTGTTTCACTGGTATGCGGGAATCC 1675
Qy 383 GCAAGGAGAACGTGGACCGCCGAGCGCGCAAGCGCGCTTGGCTTTCAGAGCGCAACG 442
Db 1676 GAAAGAGAAACGTTGATCCGCGTGAACGTGCAAAACAGGCTTAGCGTTTCGAAACGCACTG 1735
Qy 443 ACTTCGACGAGTGGCGAGCGCTGATGAGACAGAGCGCGCTGCGCGAGATGCGCGCATCC 502
Db 1736 ATTTCCAGCAGGTTCGTTTCACTCATGGAATAATAGCGATCGCTGCGAGGATATACGTAATC 1795
Qy 503 TGGCGCTTCTGCGCATCGCTTACACACCTCTGCGCATCGCGAGATCGCGCGCATCC 562
Db 1796 TGGCATTTCTGGGATGCTTATAACACCTGTTAGTATAGCCGAAATTCGAGATCA 1855
Qy 563 GCGTGAAGACATCAGCGCCAGCGCGCGCATGCTGATCCACATCGCGCGCACCA 622
Db 1856 GGGTTAAAGATATCTCACGTACTGACGTTGGGAGAAATGTTAATCCATATATGGCAGAACGA 1915
Qy 623 AGACCTTGTGAGACCGCGCGCTGAGAGAGCGCTGAGCGCTTGGCGCTGCGCGTACCAAGCTGG 682
Db 1916 AAACGCTGTTAGCACCGCAGGTGTAGAGAGGCACTTAGCGTGGGGGTAACTAAACTGG 1975
Qy 683 TGGAGCGCTGAGTACGCGTGGCGCGAGCGCGCGCATGAGCGCTTGGCGCTGCGCGTACCAAGCTGG 742
Db 1976 TCGAGCGATGGATTTCCGCTCTGCTGTAGTGTGATGATCGGATTAACCTGTTTGGC 2035
Qy 743 GCGTGCAGAAACCGCGCTGGCGCGCCCGCGCGCATGAGCGCGCGCGCGCGCGCGCGCG 802
Db 2036 GGGTCAGAAAAAATGGTGTTCGCGCCATCTGCCACAGCGAGCTATCAACTCGCGGCC 2095
Qy 803 TGGAGGCGATCTTCGAGGCGCACCCCGCGCTGATCTACCGCGCGAGGAGCGAGCGCGCG 862
Db 2096 TGGAGGCGATTTTGAAGCAACTCATCGATTGATTTACGCGCGCTAAGGATGACTCTGGTC 2155
Qy 863 AGCGCTACCTGGCTGGAGCG 922
Db 2156 AGAGATACCTGGCTGCTGAGACAGATGCGCGCTGTCGAGCGCGCGGAGATATGGCCC 2215
Qy 923 GCGCGCGCTGAGCATCCCGGAGATCATGAGCGCGCGCGCTGGAACAAAGTGAACATCG 982
Db 2216 GCGCTGGAGTTTCAATACCGAGATCATGCAAGCTGGTGGCTGGAACCAATGTAATATTG 2275
Qy 983 TGTGAACTACATCCCGAACCTTGGACAGGAGACCGCGCGCATGGTGGCGCTGCTGGAGG 1042
Db 2276 TCATGAACATATATCCGTAACCTGGATAGTGAACAGGGGCAATGGTGGCGCTGCTGGAAG 2335
Qy 1043 ACGGCGA 1049
Db 2336 ATGGCGA 2342

US-10-353-445-5

Query Match		71.9%;	Score 755;	DB 15;	Length 2346;
Best Local Similarity		83.4%;	Pred. No. 4.6e-157;		
Matches 857;		Conservative 0;	Mismatches 170;	Indels 0;	Gaps 0;
QY	23	TGAGCAACCTGTGACCGTGCACAGAACTGCGCGCCCTGCGCGTGGACGGCAGCG 82			
DB	2	TGTCCAACTGTCTACCGTTTACCAAGACCTTCGCGCTCTTCCAGTGGACGGACGTCGG 61			
QY	83	ACAGGTGGCGAAGAAGACCTGTATGGACATGTTCCGCGACCGCCAGGCTTCAGGGACCA 142			
DB	62	ATGAAGTCAGGAAGAACCTCATGGACATGTTCCGCGACAGGCAAGGTTTCAGCGACCA 121			
QY	143	CTGTGAAGATGCTGCTGAGCGTGTGCGGACGCTGGCGCCCTGCTGCTCAAGCTGAACAAC 202			
DB	122	CTGTGAAGATGCTGCTTCTCGCTGTGCGCTTCTGGGCTGATGTTGCAAGCTGAACAAC 181			
QY	203	GCAAGTGGTTCCTCCGCGAGCCGAGGACGTGCGCGACTACTGTGTACTCTGACGGCCC 262			
DB	122	CTGTGAAGATGCTGCTTCTCGCTGTGCGCTTCTGGGCTGATGTTGCAAGCTGAACAAC 181			
QY	263	GCGGCTTGGCGTGAAGACCATCCAGACGACTGGGGCCAGCTGAACATGCTGCACCGCC 322			
DB	242	GCGGGCTGGCAGTGAAGACCATCCAGCAACACCTTGGACAACCTGAACATGTTTCAGGCG 301			
QY	323	GCAGGGCTTGGCCCCCGCCCGCCAGGACGAGCAACCGCTGAGCTGTGATGCGCGGATCC 382			
DB	302	GCTCCGGCTTCCCGCGCCCGCCAGGACTCGAAGCGCGTGTGCTGATCGCGCGATCA 361			
QY	383	GCAAGGAGAACGTGGAGCGCGCGAGCGCGCCCAAGCAGGCGCTTGGCGTTCGAGCGCAAC 442			
DB	362	GGAAGGAAACGTCGATCGCGCGCGGAAAGGCAAGCAGGCGCTCGCGTTCGAGAGACCG 421			
QY	443	ACTTCGACAGGTGCGGACGCTGATGAGAAACAGCGACCGCTGCCGAGCATCCGAAC 502			
DB	422	ATTTCGACAGGTGCGGACGCTGATGAGAAACAGCGACGAGTGCAGGACATTAGAACC 481			
QY	503	TGCGCTTCTTGGCATCGCTTACAAACCTGTGCGCATCGCGAGATCGCCCGCATCC 562			
DB	482	TGGGTTCTTCGGAATTGCAATACACACGCTCTCAGGATCGGGAATTTGCCCGCATTC 541			
QY	563	CGGTGAAGGACATCAGCGCGACCGCGCGCGCGCATGTGATCCACATCGCGCGCACCA 622			
DB	542	CGGTGAAGGACATTTAGCGCACCGACCGCGCGCGAGATGCTTATCCATTTGGCAGGACCA 601			
QY	623	AGACCTTGTGAGACCGCGCGCGTGTGAGAAAGCCCTGAGCTGGGCGTGAACAACTGG 682			
DB	602	AGACGCTCGTTTCCACCGCGAGCGGTGAAAAGGCGCTTCAGCGCTCGGAGTGACCAAGCTCG 661			
QY	683	TGGAGCGCTGATCAGCGGTGAGCGCGTGGCGCGACGACCCCAACAACTACTGTTCTGCC 742			
DB	662	TCGACGCTGGAATCTCGTGTCCGCGTTCGCGGACGACCCCAACAACTACTCTTCTGCC 721			
QY	743	CGGTGCGCAAGAACGGCGTGGCGCCCGCCAGCGCCACAGCCAGCTGAGCACCGCGGCC 802			
DB	722	CGGTGCGCAAGAACGGCGTGGCTGCCCTTAGCGCCACAGCCAACTCAGCACGAGGGCGCT 781			
QY	803	TGGAGGGCATCTTGGAGGCAACCCACGCGCTGATCTAGCGCGCCCAAGGACGACGCGGCC 862			
DB	782	TGGAAGGTATTTTCGAGGCGCAACCCACGCGCTGATCTAGCGCGCCCAAGGATGACGCGGTC 841			
QY	863	AGCGCTACTCGCTGGAGCGGCGCACAGCGCGCGCGTGGGCGCGCGCGACATGCGGCC 922			
DB	842	AACGCTACTCGATGTTCCGGGCACTCCGCGCGCGTGGAGCTGTAGGACATGCGGCC 901			
QY	923	GCGCGCGGTGAGCATCCCGAGATCATGAGGCGCGCGGTGAGCAACAACTGAACATCG 982			
DB	902	GCGCGCGGTGTTTCATCCCGGAAATCATGCGAGCGGCTGGATGACGAACGCTGAACATG 961			
QY	983	TGATGAATCATATCCGCAACTGAGACGAGCGAGACGCGGCGCATGTTGCGCTTCTGGAGG 1042			
DB	962	TCATGAATCATATTCGCAACCTTGACAGCGAGACGCGGCGCAATGTTGCGCTTCTGGAGG 1021			

RESULT 2

US-10-353-445-2
; Sequence 2, Application US/10353445
; Publication No. US20030119166A1
; GENERAL INFORMATION:
; APPLICANT: Baszczynski, Christopher L.
; APPLICANT: Lyznik, Leszek A.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Guan, Xueni
; APPLICANT: Rao, Guru
; APPLICANT: Tagliani, Laura A.
; TITLE OF INVENTION: A No. US20030119166A1 Method For The Integration Of Foreign Di
; FILE REFERENCE: 5718-66 (amended listing)
; CURRENT APPLICATION NUMBER: US/10/353,445
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US/09/193,503B
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1032
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: sequence encoding Cre protein from Bacteriophage
; OTHER INFORMATION: P1, maize preferred codons (moCRE)
US-10-353-445-2

Query Match 71.8%; Score 754.4; DB 15; Length 1032;
Best Local Similarity 83.4%; Pred. No. 6.5e-157;
Matches 857; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

QY	23	TGAGCAACCTGTGACCGTGCACAGAACTGCGCGCCCTGCGCGTGGACGGCAGCG 82	
DB	2	TGTCCAACTGTCTACCGTTTACCAAGACCTTCGCGCTCTTCCAGTGGACGGACGTCGG 61	
QY	83	ACAGGTGGCGAAGAAGACCTGTATGGACATGTTCCGCGACCGCCAGGCTTCAGCGAGCACA 142	
DB	62	ATGAAGTCAGGAAGAACCTCATGGACATGTTCCGCGACAGGCAAGGTTTCAGCGAGCACA 121	
QY	143	CTGTGAAGATGCTGCTGAGCGTGTGCGGACGCTGGCGCGCTGCTGCTGCTGAACAAAC 202	
DB	122	CTGTGAAGATGCTGCTTCTCGCTGTGCGCTTCTGGGCTGATGTTGCAAGCTGAACAAC 181	
QY	203	GCAAGTGGTTCCTCCGCGAGCCCGAGGAGTGTGCGCGACTACTGTGTACTCTGACGGCCC 262	
DB	182	GGAAGTGGTTCCTCCGCTGAGCCCGAGGACGTTGAGGATTAACCTTCTGTACTGCAAGCTC 241	
QY	263	GCGGCTTGGCGTGAAGACCATCCAGACGACTGGGGCCAGCTGAACATGCTGCACCGCC 322	
DB	242	GCGGGCTGGCAGTGAAGACCATCCAGCAACACCTTGGACAACCTGAACATGTTTCAGGCG 301	
QY	323	GCAGGGCTTGGCCCCCGCCCGCCAGGACGAGCAACCGCTGAGCTGTGATGCGCGGATCC 382	
DB	302	GCTCCGGCTTCCCGCGCCCGCCAGGACTCGAAGCGCGCTGAGCTTCGTATGCGCGCATCA 361	
QY	383	GCAAGGAGAACGTGGAGCGCGAGCGCGCCCAAGCAGGCGCTTGGCGTTCGAGCGCAAC 442	
DB	362	GGAAGGAAACGTCGATCGCGCGCGGAAAGGCAAGCAGGCGCTCGCGTTCGAGAGACCG 421	

QY 443 ACTTCGACCAAGTCCGAGCCTGATGAGAAACAGCGACCGCTGCCAGGACATCCGCAACC 502
DB 422 ATTTTCGACCAAGTCCGAGCCTGATGAGAAACAGCGACAGGTGCCAGCAATTAGGAACC 481
QY 503 TGGCCTTCTCTGGGATCGCCTACCAACACCTGCTGGCATCGCGAGATCGCCCGCATCC 562
DB 482 TGGCGTTCTCTGGAAATTGCAATACACACGCTCTCTCAGGATCGCGGAAATTTGCCCGCATTC 541
QY 563 GCGTGAAGGACATCAGCGGCACCGACCGCGCGCGCATGCTGATCCACATCGCGCGCACCA 622
DB 542 GCGTGAAGGACATTTAGCGGCACCGACCGCGCGCAGATGCTTATCCATTTGGCAGGACCA 601
QY 623 AGACCTCTGTGAGCACCGCGCGCTGGAGAAAGGCCCTGAGCCTGGCGGTGACCAAGCTGG 682
DB 602 AGACGCTCGATTTCACCGCAGCGCTCGAAAGGCCCTCAGCCTCGGAGTGACCAAGCTCG 661
QY 683 TGGAGCGCTGATCAGCGGTGAGCGGCTGGCGGCGGCGGACCCCAACATCTACTGTTCTGCC 742
DB 662 TCGAACGCTGATCTCCGTTGTCGCGGCTGCGGAGCAGACCCCAACATCTACTGTTCTGCC 721
QY 743 GCGTGGCAGAAACGGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 802
DB 722 GCGTGGCAGAAACGGGTGGCTGCGCTAGCGGCGACCGACCACTCAGCACGAGGCGCT 781
QY 803 TGGAGGGCATCTTCGAGGCCACCCACCGCCTGATCTACGGCGGCCAAGACGACGCGCC 862
DB 782 TGGAAAGTATTTTCGAGGCCACCCACCGCCTGATCTACGGCGCGAAGGATGACAGCGGTC 841
QY 863 AGCCTACCTGGCTGGAGCGGCGCACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 922
DB 842 AACGCTACCTGGCATGCTCGCGGCGACTCGCGCGCGCTGGAGCTGCTAGGGACATGGCC 901
QY 923 GCGCGGCGTGGAGCATCCCGAGATCATGACAGCGCGCGCGCGCGCGCGCGCGCGCGCG 982
DB 902 GCGCGGCTGTTTCCATCCCGAATCATGCAAGCGGCTGGATGACGAACTGAACTTG 961
QY 983 TGATGAATACATCCGAACCTGGACAGCGAGACCGCGCGCGCGCGCGCGCGCGCGCGCG 1042
DB 962 TCATGAATACATTCGAACTTCACAGCGAGACGCGCGCGCAATGTTCTCGCCTCTCGAAG 1021
QY 1043 ACGCGGAC 1050
DB 1022 ATGGTGAC 1029

RESULT 3

US-09-948-193-2
; Sequence 2, Application US/09948193
; Publication No. US20030027335A1
; GENERAL INFORMATION:
; APPLICANT: Ruley, H. Earl
; APPLICANT: Jo, Daewoong
; TITLE OF INVENTION: Genome Engineering by Cell-Permeable DNA
; TITLE OF INVENTION: Site-Specific Recombinases
; FILE REFERENCE: 22000.0109U2
; CURRENT APPLICATION NUMBER: US/09/948,193
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/230,690
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description: His6-NLS-Cre-MTS
US-09-948-193-2

Query Match 60.9%; Score 639.4; DB 11; Length 1158;
Best Local Similarity 75.6%; Pred. No. 1.2e-131;
Matches 793; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

QY 1 ATGCCCAAGAGAGGAAAGTGAACAACCTCTGACCGTGCACCAAGAACCTGCCCGCC 60
DB 61 ATGCCCAAGAGAGGAAAGTGTCCAATTTACTGACCGTACACCAAAATTTGCTGTCA 120
QY 61 CTGCCGTGACGCCACCGACGAGGTGCGCAAGAACCTGATGACATGTTCCCGGAC 120
DB 121 TTACCGGTGATGCAACAGAGTGTGCGAAGAACCTGATGACATGTTTCCGGAT 180
QY 121 CGCAGCGCTTACGCGAGCACACTGGAAGATGCTGCTGAGCGTGTGCCCGAGCTGGCC 180
DB 181 GCGCAGCGCTTCTTGAGCATACCTGGAATAATGCTTCTGTCCGTTTCCCGGTGTTGGCG 240
QY 181 GCCTGTGTGAAGTGAACAAACCGCAAGTGTTCCTCCCGCGAGGCCGAGGACGTCGCGAC 240
DB 241 GCATGTGTGCAAGTGAATAACCGGAAATGTTTCCCGCAGAACTCTGAAGATGTTCCGAT 300
QY 241 TACTGTGTGCTGAGCGCGCGCGCTGGCGTGAAGACCATCCAGGACGACCTGGCC 300
DB 301 TATCTTCTATCTTCTGAGCGCGCGCTGCGCAGTAAAACTATCCAGCAACATTTGGGC 360
QY 301 CAGCTGAACATGCTGACCGCGCGCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCG 360
DB 361 CAGCTGAACATGCTTCTGCTCGTCCGCGTGCAGCAGCAAGTGAACATGCTGTT 420
QY 361 AGCCTGTGTGATGCGCGCATTCGCAAGGAGAACGTTGACCGCGCGCGCGCGCGCGCG 420
DB 421 TCAGTGTGTATGCGCGGATCCGAAAGAAAAAGTGTGATCCCGGTGAACGTCGCAAAACAG 480
QY 421 GCCTGTGCTTTCGAGCGCACCGACTTCGACAGGTGGCGGACCTGATGAGAACAGCGAC 480
DB 481 GCTCTAGCGTGTGAACGCGACTGTTTCGACAGGTTCGTTTCACTCATGGAATAATAGCGAT 540
QY 481 CGCTGCGAGACATCCGCAACCTGGCGTTCCTGGGCATCGCTTACCAACACCTGCTCGCG 540
DB 541 CGCTGCGAGATATACGTAATCTGGCATTTCTGGGATGCTTATAACACCTGTTACGT 600
QY 541 ATCCCGAGATTCGCGCGCATCCGCGTGAAGGACATCAGCCGCGCACCGCGCGCGCGCATG 600
DB 601 ATAGCGAAATTCGCGAGATCAGGTTAAAGATATCTCACGTACTGACGCTGGGAGAAATG 660
QY 601 CTGATCCATATGCGCGCACCAAGACCTGTGAGGACCGCGCGCGTGGAGAGAGCGCTG 660
DB 661 TTAATCCATATGCGAGAACGAAACGCTGTTTAGCACCGCAGGTGTAGAGAGGCACTT 720
QY 661 AGCCTGGCGTGCACCAAGCTGTGGAGCGTGGATCAGCGTGAAGCGCGTGGCGGACGAC 720
DB 721 AGCCTGGGGTAACTAACTGGTCGAGCATGGAATTCCTGCTCTGTTGTAGCTGAT 780
QY 721 CCCAACAACTACCTGTTCTGCGCGTGCAGAAACCGCGCTGGCGCGCGCGCGCGCGCAC 780
DB 781 CCGAATAACTACCTGTTTTCGCGGTTCAGAAAAATGTTGTGCGCGCATCTGCCACC 840
QY 781 AGCAGCTGAGCACCGCGCGCTGGAGGATCTTGGAGGCACTTCCAGCGCATCTATCTAC 840
DB 841 AGCAGCTATCACTCGCGCGCTGGAAGGATTTTGAAGCACTCATCGATTGATTAC 900
QY 841 GCGGCCAAGGACGACGCGCGCTACTGCGCTGGAGCGCGCGCGCGCGCGCGCGCGGTG 900
DB 901 GCGCTAAGGATGACTCTGTCAGAGATACCTGGCGTGGTGTGACACAGTGGCGCGGTG 960
QY 901 GCGCGCGCGCGCACATGGCGCGCGCGGTGAGCATCCCGAGATCATGACGCGCGCG 960
DB 961 GGAGCGCGCGAGATATGGCGCGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGGT 1020
QY 961 GGTGGACCAACGTTGAACATGTTGATGAATCACTCGCAACCTGGACAGGACGCGCG 1020
DB 1021 GGTGGACCAATGTTGAATATTTGTCATGAACTATATATCGTAACCTGGATAGTGAACAGGG 1080
QY 1021 GCATGTGTGCGCTGCTGGAGGACGCGCA 1049
DB 1081 GCAATGTGTGCGCTGCTGGAGATGGCGCA 1109

RESULT 4
US-09-916-780A-2
; Sequence 2, Application US/09916780A
; Patent No. US20020124280A1
; GENERAL INFORMATION:
; APPLICANT: University of Connecticut
; APPLICANT: Li, Yi O'Donnell, Colum Wu, Yan McAvoy, Richard
; TITLE OF INVENTION: Methods for the Controlled, Automatic Excision of Heterologous DN
; TITLE OF INVENTION: Transgenic Plants and DNA-Excising Gene Cassettes for Use Therein
; FILE REFERENCE: 883933.0066
; CURRENT APPLICATION NUMBER: US/09/916,780A
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/221,318
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1553
; TYPE: DNA
; ORGANISM: Bacteriophage P1
US-09-916-780A-2

Query Match 58.9%; Score 618.4; DB 10; Length 1553;
Best Local Similarity 74.8%; Pred. No. 5.1e-127;
Matches 775; Conservative 0; Mismatches 261; Indels 0; Gaps 0;

QY 14 AGAGGAGGTGAGCAACCTGCTGACCGTGCACGAGCAACCTGCCCGCTCCCGTGGAGC 73
DB 477 AGTGTAAATGTCATTTACTGACCGTACACCAAAATTTGCTGCAATACCGTGCATG 536

QY 74 CCACGACGAGGTGCGCAAGAACCTGATGACATGTTCCGCGACCGCCAGCCCTTCA 133
DB 537 CAACGAGTGATGAGTTGCGAAGAACCTGATGACATGTTTCCAGGATGCGCAGCGTTT 596

QY 134 GCGAGCACCTGGAAGATGCTGCTGAGCGTGTGCCGACGCTGGCGCGCTGTCGAGC 193
DB 597 CTGAGCATACCTGGAATAATGCTTCTGTCCTGTTGCCGCTGTCGGCGGCATGTTGCAAGT 656

QY 194 TGAACACCCAGTGTGTTCCCGCCGAGCCGCGAGGAGTGGCGACTGCTGTGATGC 253
DB 657 TGAATAACCGGAATGTTTCCCGCAGAACCTGGAAGATGTTTCGCGATATCTTCTATATC 716

QY 254 TGACGCGCCGCGGCTCGCGCTGAAGACCATTCAGCAGCAGCTGGGCGAGCTGAACATGC 313
DB 717 TCCAGCGCGCGTCTGCGAGTAAACTATCCAGCAACATTTGGGCGCAGCTAAACATGC 776

QY 314 TGACCGCCGAGCGGCTGCGCGCCGAGCCGCGAGGAGTGGCGACTGCTGTGATGC 373
DB 777 TCCATCGCTCGTCCGGGCTGCGCAGCAAGTGAAGCAATGCTGTTTCACTGGTTATGC 836

QY 374 GCGCATCCGCAAGGAGAACTGACGCGCGCGAGCGCGCAAGCAGCGCTGCGCTTCG 433
DB 837 GCGGATCCGGAAGAAAGAAAGTTGATGCGCGTGAACGTGCAAAACAGGCTCTAGCGTTCG 896

QY 434 AGCGCAACGATTCGACAGGTGCGCAGCCTGATGAGAAACAGCAGCGCTGCCAGGACA 493
DB 897 AACGCACTGATTTGCAACAGTTTCTCACTCATGGAATAAGCATGCTGCCAGGATA 956

QY 494 TCCGCAACCTGCGCTTCTGGGATGCTTCAACACCTGCTGCGCATGCCGAGATCG 553
DB 957 TACGTAATCTGGCAATTTCTGGGATGCTTATAACACCTGTTACGTATAGCCGAAATG 1016

QY 554 CCGCATCCGCTGAAGGACATACGCGCACCGCGCGCGCGCATGCTGATCCACATCG 613
DB 1017 CCAGATCAGGTTTAAAGATATCTACGTACTGACGTTGGAGAAATGTTATCCATATG 1076

QY 614 GCGGACCAAGACCTGTTGAGCACCGCGCGCGTGGAGAAAGCGCTGAGCCTGGCGCTGA 673
DB 1077 GCAGAACGAAACCGTGGTAGCCGCGAGGTGTAGAGAGGCACTTAGCCTGGGGTAA 1136

QY 674 CCAAGCTGGTGGAGCGCTGGAATCAGCGTGAAGCGGCGTGGCGAGCAACCAACTACC 733

DB 1137 CTAAACTGGTCGAGCGATGGATTTCCGTCTCTGGTGTAGTGATGATCGAATAACTACC 1196

QY 734 TGTCTTCCCGCTGCGCAAGAACGCGTGGCGCGCCCCCAGCGCCACACCGAGCTGAGCA 793
DB 1197 TGTCTTCCCGCTGCGCAAGAACGCGTGGCGCGCCCCCAGCGCCACACCGAGCTATCAA 1256

QY 794 CCGGCGCTTGGAGGCACTTTCGAGGCAACCGCCGCTGATCTACGGCGCAAGGAGC 853
DB 1257 CTCGCGCTTGAAGGGATTTTGAAGCAACTCATCGATTGATTACGCGCTAAGGATG 1316

QY 854 ACAGCGCGCAGCGCTACCTGGCGCTGAGCGGCCACAGCGCCCGCTGGCGCGCGCGCG 913
DB 1317 ATCTTGGTCAGAGATACCTGGCGCTGGTCTGGACACAGTGGCGCTGCGAGCGCGCG 1376

QY 914 ACATGCGCGCGCGCGGTGAGCATCCCGAGATCATGCGAGCGCGCGCTGCGACCAAG 973
DB 1377 ATATGCGCGCGCTGGAGTTTCAATACCGAGATCATGCAAGCTGGTGGCTGGACCAATG 1436

QY 974 TGAACATCGTGTGAACTACATCCGCAACCTGAGCAGCGCGCGCATGTTGGCGC 1033
DB 1437 TAAATATTGTCATGAACATATATCCGTAACTGATAGTGAACAGGGCAATGGTGGCGC 1496

QY 1034 TGCTGGAGGACGCGCA 1049
DB 1497 TGCTGGAAGATGCGCA 1512

RESULT 5
US-09-880-107-3674
; Sequence 3674, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3674
; LENGTH: 1553
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X03453
US-09-880-107-3674

Query Match 58.9%; Score 618.4; DB 10; Length 1553;
Best Local Similarity 74.8%; Pred. No. 5.1e-127;
Matches 775; Conservative 0; Mismatches 261; Indels 0; Gaps 0;

QY 14 AGAGGAGGTGAGCAACCTGCTGACCGTGCACGAGCAACCTGCCCGCTCCCGTGGAGC 73
DB 477 AGTGTAAATGTCATTTACTGACCGTACACCAAAATTTGCTGCAATACCGTGCATG 536

QY 74 CCACGACGAGGTGCGCAAGAACCTGATGAGCATGTTTCCGCGACCGCGCTGTCGAGC 133
DB 537 CAACGAGTGATGAGTTGCGAAGAACCTGATGACATGTTTCCAGGATGCGCAGCGCTTT 596

QY 134 GCGAGCACCTGGAAGATGCTGCTGAGCGTGTGCCGAGCTGGCGCGCTGTCGAGCAGC 193
DB 597 CTGAGCATACCTGGAATAATGCTTCTGTCCTGTTTGGCGTGTGGCGGCGCATGTTGCAAGT 656

QY 194 TGAACACCCAGTGTGTTCCCGCGCGAGCCGCGAGGAGCGTGGCGCACTACTGCTGTGATC 253
DB 657 TGAATAACCGGAATGTTTCCCGCGAGAACCTGGAAGTGTTCGCGATATCTTCTATATC 716

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QY 254 TGCAGCCCGCGGCTGGCGGTGAAGACCATCCAGCAGCACCTTGGCGCAGCTGAACATGC 313
Db |||||
QY 717 TTCAGGCGCGGGTCTGGCAGTAAAACTATCCAGCAACATTTGGGCGCAGCTAAACATGC 776
Db |||||
QY 314 TGCACCCCGCAGCGGGCTGCCCGCCCCCAGCAGCAGCAACGCGCTGAGCTGTGTATGC 373
Db |||||
QY 777 TTCATCGTGGTCCGGGCTGCCAGCAACAGTGAACAGTATGCTGTTTCACTGGTTATGC 836
Db |||||
QY 374 GCGGCATCCGAAAGGAGAACGTGAGCCGCGCGAGCGCGCAAGCAGCGCCTGGCCTTCG 433
Db |||||
QY 837 GCGGCATCCGAAAGGAGAACGTGAGCCGCGGTGAACGTGCAAAACAGGCTCTAGCGTTGC 896
Db |||||
QY 434 AGCAGCCGACTTCGACAGTGGCGAGCCTGATGGAGACAGCAGCGCTGCCAGACA 493
Db |||||
QY 897 AACGCACTGATTCGACAGGTTTGTTCACTCATGGAATAAGCAGTGGTCCAGGATA 956
Db |||||
QY 494 TCCGCAACCTTGGCCCTTCTGGGCGATCGCTCAACACACCTCTCGCATGCGCCAGATCG 553
Db |||||
QY 957 TAGGTATCTGGCATTTCTGGGATTTGCTTATACACCCCTGTACGTATAGCCGAATTG 1016
Db |||||
QY 554 CCGGCATCCGCGTGAAGAACATCAGCCGCAACGAGCGCGCGCGCATGCTGATCCACATCG 613
Db |||||
QY 1017 CCAGGATCAGGGTTAAAGATATCTCAGCTACTGACCGGTGGAGAAATGTTAATCCATATG 1076
Db |||||
QY 614 GCGCAGCAGACCTTGGTGAAGCAGCGCGCGGTGGAGAGCGCCTGAGCTGGCGGTGA 673
Db |||||
QY 1077 GCAGAACGAAACCGCTGGTAGCAGCGCAGGTGTAGAGAGGCGCACTTAGCGCTGGGGTAA 1136
Db |||||
QY 674 CCAAGCTGGTGGAGCGCTGAGTCAAGCGTGAAGCGCGTGGCGAGCAGCCCAACAACTACC 733
Db |||||
QY 1137 CTAACTGGTTCAGCGATGGATTTCCGTTCTGTGTAGCTGATGATCCGATTAACCTACC 1196
Db |||||
QY 734 TGTTCTGCGCGTCCGCAAGAACCGCGTGGCGCGCCCCCAGCGCACACAGCCAGCTGAGCA 793
Db |||||
QY 1197 TGTTTTCGCGGTGAGAAAAATGGTGTGGCGCGCATCTGCCAGCAGCTATCAA 1256
Db |||||
QY 854 ACAGCGCCAGCGCTACTCTGGCTGGAGCGGCCACAGCGCGCGTGGCGCGCGCGCG 913
Db |||||
QY 1317 ACTCTGTTCAGAGATACCTGGCTTGTGACACAGTGCCTGTCGAGCGCGCGAG 1376
Db |||||
QY 914 ACATGGCCCGCGCGGTGAGCATCCCGAGATCATCGAGCGCGCGGTGGACCAACG 973
Db |||||
QY 1377 ATATGGCCCGCGTGGAGTTTCAATACCGGAGATCATGCAAGCTGGTGGTGGACCAATG 1436
Db |||||
QY 974 TGAACATCGTGAATGATATCCGCAACCTGGACAGCGAGACCGCGCCATGTTGCGCC 1033
Db |||||
QY 1437 TAAATATTGATGAATATATCCGTAACTTGGATGTGTAACAGGGGCAATGTTGCGCC 1496
Db |||||
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RESULT 6

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US-09-948-193-8
; Sequence 8, Application US/09948193
; Publication No. US20030027335A1
; GENERAL INFORMATION:
; APPLICANT: Ruley, H. Earl
; APPLICANT: Jo, Daewoong
; TITLE OF INVENTION: Genome Engineering by Cell-Permeable DNA
; TITLE OF INVENTION: Site-Specific Recombinases
; FILE REFERENCE: 22000.0109U2
; CURRENT APPLICATION NUMBER: US/09/948,193
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/230,690
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 21
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1553
; TYPE: DNA
; ORGANISM: Bacteriophage P1
; FEATURE:
; OTHER INFORMATION: Description: gene encoding Cre recombinase
US-09-948-193-8
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Query Match 58.9%; Score 618.4; DB 11; Length 1553;
Best Local Similarity 74.8%; Pred. No. 5.1e-127;
Matches 775; Conservative 0; Mismatches 261; Indels 0; Gaps 0;
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QY 14 AGAGGAAGTGAAGCAACCTCTGACCGTGACCGTGACCGCAACCTGCGCGCGCTGCCGTGAACG 73
Db |||||
QY 477 AGTGTAAATGTCCAATTTACTGACCGTACACCAAAATTTGCTGTGATTAACCGTGCATG 536
Db |||||
QY 74 CCACACGACGAGAGGTGCGCAAGAACTGATGATGACATGTTCCGCGAGCCGCGCGCCTTCA 133
Db |||||
QY 537 CAACGAGTGAAGGTTCGCAAGAACCTGATGACATGTTTCAGGGATTCGCCGCGCTTT 596
Db |||||
QY 134 GCGAGCACACCTTGAAGATGCTGCTGAGCGTGTGCCGAGCTGGCGCGCTGTGTGCAAGC 193
Db |||||
QY 597 CTGAGCATACCTGGAAAAATGCTTCTGTCCGTTTGGCGGTGCGGCGCATGGTGAAGT 656
Db |||||
QY 194 TGAACAAACCGAAGTGGTTCGCCCGAGCCCGAGGACGTCGCGCATCTCTGCTGTACC 253
Db |||||
QY 657 TGAATAACCGAAATGGTTCGCCGAGAACCTGAAGATGTTTCGCGATTTCTTCTATATC 716
Db |||||
QY 254 TGCAGGCGCGCGCTGGCGTGAAGAACCATCCAGCAGCACCTGGGCGCAGCTGAACATGC 313
Db |||||
QY 717 TTGAGGCGCGCGTCTGGCAGTAAACCTATCCAGCAACATTTGGGCGCAGCTAAACATGC 776
Db |||||
QY 314 TGCACCGCGCAGCGCGCTGCCCGCCAGCAGCACAGCGCGTGAAGCTGTGATGC 373
Db |||||
QY 777 TCCATCGTGGTCCGGCTGCCAGCAAGTGAAGCAATGCTGTTCACTGTTATGC 836
Db |||||
QY 374 GCGCATCCGCAAGGAGACGTGAGCGCGCGAGCGCGCAAGCAGCGCCTGGCCTTCG 433
Db |||||
QY 837 GCGCGATCCGAAAGAAAAAGTGGTGGTGGCGGTGAAGCTGCAAAACAGGCTTAGCGTTCG 896
Db |||||
QY 434 AGCGCACCGACTTTCGACAGGTGCGCAGCTGATGGAGACAGCGCGCTGCCAGACA 493
Db |||||
QY 897 AACGCACTGATTTTCGACAGGTTCGTTCACTCATGGAATAAGCAGTTCGCGCGAGATA 956
Db |||||
QY 494 TCCGCAACCTTGGCCTTCTTGGCGATCGCTTAAACACCTGTGTCGCGCATCGCGAGATCG 553
Db |||||
QY 957 TAGGTATCTGGCATTTCTGGGATTTGCTTAAACACCTGTACGTATAGCCGAATTCG 1016
Db |||||
QY 554 CCGCATCCGCGTGAAGGACATCAGCGCGCACCGCGCGCGCGCGCGCATGCTGATCCACATCG 613
Db |||||
QY 1017 CCAGGATCAGGGTTAAAGATATCTCAGCTACTGACCGTGGGAGAAATGTTAATCCATATG 1076
Db |||||
QY 614 GCGCGACCAAGACCTTGTGAGCACCGCGCGTGGAGAGCGCCTGAGCCTGGCGGTGA 673
Db |||||
QY 1077 GCAGAACGAAACCGTGGTTAGCAGCGAGGTGAGAGAGGCACCTTAGCTGGGGTAA 1136
Db |||||
QY 674 CCAAGCTGGTGGAGCGCTGATCAGCGTGAAGCGCGTGGCGCAGCAGCCCAACAACTACC 733
Db |||||
QY 1137 CTAACTGGTTCGAGCGATGATTTCCGTTCTGTGTAGCTGATGATCCGATTAACCTACC 1196
Db |||||
QY 734 TGTTCTGCGCGTCCGCAAGAACGCGGTGCCCGCCCCCAGCGCACACAGCCAGCTGAGCA 793
Db |||||
QY 1197 TGTTTTCGCGGTGAGAAAAATGGTGTGGCGCGCATCTGCCAGCAGCTATCAA 1256
Db |||||
QY 794 CCGCGCGCTTGGAGGCGATCTTCGAGCGCACCGCGCTGATCTAGGCGCGCAGGACG 853
Db |||||
QY 1257 CTCGCGCGCTGGAAGGATTTTGAAGCAACTCATCGATTTAGTTTTCGCGCGCTAAGGATG 1316
Db |||||
QY 854 ACAGCGCCAGCGCTACTCTGGCTGGAGCGGCCACAGCGCGCGTGGCGCGCGCGCG 913
Db |||||
QY 1317 ACTCTGTTCAGAGATACCTGGCTTGTGACACAGTGCCTGTCGAGCGCGCGAG 1376
Db |||||
QY 914 ACATGGCCCGCGCGGTGAGCATCCCGAGATCATCGAGCGCGCGGTGGACCAACG 973
Db |||||
QY 1377 ATATGGCCCGCGTGGAGTTTCAATACCGGAGATCATGCAAGCTGGTGGTGGACCAATG 1436
Db |||||
QY 974 TGAACATCGTGAATGATATCCGCAACCTGGACAGCGAGACCGCGCCATGTTGCGCC 1033
Db |||||
QY 1437 TAAATATTGATGAATATATCCGTAACTTGGATGTGTAACAGGGGCAATGTTGCGCC 1496
Db |||||
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QY 914 ACATGGCCGCGCGCGGTGAGCATCCCGAGATCATGAGCGCGCGGTGACCAACG 973
Db 1377 ATATGGCCGCGGTGAGTTTCAATACCGGAGATCATGCAAGCTGGTGGCGACCAATG 1436
QY 974 TGAACATCGTGATGAACATACATCCGAACCTGGACACGAGACCGCGCGCATGGTGGCC 1033
Db 1437 TAATATTGTCAGAACTATATCCGTAACTGGATAGTAGTAAACAGGGGCAATGGTGGCC 1496
QY 1034 TGCTGGAGGACGGCA 1049
Db 1497 TGCTGGAAGATGGCA 1512
RESULT 7
US-10-252-279-2
; Sequence 2, Application US/10252279
; Publication No. US20030190746A1
; GENERAL INFORMATION:
; APPLICANT: Xiao Xiao
; APPLICANT: Xiao Xiao
; TITLE OF INVENTION: GENE EXPRESSION CONTROL SYSTEM AND ITS USE IN RECOMBINANT VIRUS
; FILE REFERENCE: 020059
; CURRENT APPLICATION NUMBER: US/10/252,279
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/369,987
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1553
; TYPE: DNA
; ORGANISM: Bacteriophage P1
US-10-252-279-2

Query Match 58.9%; Score 618.4; DB 13; Length 1553;
Best Local Similarity 74.8%; Pred. No. 5.1e-127;
Matches 775; Conservative 0; Mismatches 261; Indels 0; Gaps 0;

QY 14 AGAGGAAGTGAGCAACCTGTCACCGTGCACCAAGAACCTGCCCGCCCTGCCGTGGACG 73
Db 477 AGTGTAAATGTCCTCAATTTACTACCGTACACCAAAATTTGCTGTCATTACCGGTGATG 536
QY 74 CCACGACGAGGTGGCGAGAACCTGATGACATGTTCCGCGACCGCGAGCCCTTCA 133
Db 537 CAACGAGTGTAGAGTTTCGAAGAACCTGATGGACATGTTTCAGGGATCGCGCGCTTT 596
QY 134 GCGAGCACCTGGAAGATGCTGCTGAGCGTGTCCGCGAGCTGGCGCGCTGGTGAAGC 193
Db 597 CTGAGCATCTGGAATAATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 656
QY 194 TGAACAAACCGAAGTGGTTCCCGCGAGCCGAGCGAGCGAGTGCAGCTACTGCTGTACC 253
Db 657 TGAATAACCGAATAAGTTTCCCGCGAGAACCTGAAGATGTTTCGCGATTATCTTCTATATC 716
QY 254 TGCAGCGCGCGCGCTGGCGTGAAGACCATCGAGAGACCTGGCGCGAGCTGACATGC 313
Db 717 TTCAGGCGCGCGTCTGCGAGTAAATACTATCCAGCAACATTTGGGCGAGCTAAACATGC 776
QY 314 TGACCGCGCGAGCGGCTGCCCGCCCGCGAGCGAGCAACGCGCTGAGCTGTGTATGC 373
Db 777 TTTATGCTGCTGCGGCTGCCAGACCAAGTGAAGATGCTGTTTCTGTTTATGC 836
QY 374 GCGGCATCCGCAAGGAGAACCTGGACGCGCGCGAGCGCGCAAGCAGCGCCCTGSCCTTCG 433
Db 837 GCGGCATCCGAAAGAAACCTGTATGCGCGTGAACCTGCAAAACAGGCTCTAGCGTTG 896
QY 434 AGCGACCGACTTCGACAGGTGGCGAGCTGTATGAGAAACAGCGACCGGTGCCAGACA 493
Db 897 AACGCACTGATTTGACGAGGTTCGTTCACTCATCTGAAATATAGCATCGCTGCCAGGATA 956
QY 494 TCCGCAACCTGGCGCTTCCTGGGCTATCGCTACACACCTGCTGCGCATCGCGAGATCG 553

Db 957 TACGTAATCTGSCATTTCTGGGGATTGCTTATAACACCTGTTACGTATAGCGAAATTG 1016
QY 554 CCGCATCCGCGTGAAGACATCAGCCGACCGAGCGCGCGCATGCTGATCCACATCG 613
Db 1017 CCAGGATCAGGGTTAAAGATACTCAGCTACTGACGGTGGGAGAAATGTTAAATCCATATTG 1076
QY 614 GCGCACCAAGACCTGCTGAGCAGCGCGGTGGAGAGCCCTGAGCCTGGCGCTGA 673
Db 1077 GCAGAACGAAACCGCTGGTTAGCAGCGAGGTGTAGAGAAAGCACTTAGCCTGGGGGTAA 1136
QY 674 CCAAGCTGCTGAGCGCTGGATCAGCTGAGCGGTGGCCGACGACCCCAACAACTACC 733
Db 1137 CTAAACTGCTCGAGCATGATTTCCGCTCTCTGGTGTAGTGTATGATCCGATTAATACC 1196
QY 734 TGTCTGCGCGTGGCGCAAGAACGCGTGGCGCGCCCGCCAGCGCCAGCCAGCTGAGCA 793
Db 1197 TGTCTTTCGCGGTTCAGAAAAAATGTTGTCGCGCGCATCTGCACAGCCAGCTATCAA 1256
QY 794 CCGGGCCCTGGAGGCGCATCTTCGAGGCCACCCACCGCTGATCTACGGCGCCAGGACG 853
Db 1257 CTCGCGCCTGGAAGGATTTTGAAGCAACTCATCGATTGATTACGGCGCTAAGGATG 1316
QY 854 ACAGCGCCAGCGCTACCTGGCTTGGAGCGGCGCACAGCCCGCGTGGCGCGCCCGCG 913
Db 1317 ACTCTGCTCAGAGATACCTGGCTGGTCTGGACACAGTGCCTGTCGAGCGCGCGAG 1376
QY 914 ACATGCGCGCGCGCGGTGAGATCCCGAGATCATGAGCGCGCGCTGAGCAACAG 973
Db 1377 ATATGCGCGCGCTGGAGTTTCAATACCGAGATCATGCAAGCTGCTGCTGAGCAATG 1436
QY 974 TGAACATCGTGAATACATACCTCCGCAACCTCGACAGCGAGACCGCGCATGGTGGCC 1033
Db 1437 TAAATATTGTCATGAACATATATCCGTAACCTGATAGTAAACAGGGGCAATGGTGGCC 1496
QY 1034 TGCTGGAGGACGGCGA 1049
Db 1497 TGCTGGAAGATGGCA 1512

RESULT 8

US-10-097-554A-5
; Sequence 5, Application US/10097554A
; Publication No. US20030170642A1
; GENERAL INFORMATION:
; APPLICANT: Jeremy Scot Caldwell
; APPLICANT: Sumit K. Chanda
; APPLICANT: Nikunj V. Somia
; APPLICANT: John B. Hogenesch
; APPLICANT: Michael P. Cooke
; APPLICANT: Pedro Aza-Blanc
; TITLE OF INVENTION: IDENTIFICATION OF CELLULAR TARGETS FOR BIOLOGICALLY ACTIVE MOLE
; FILE REFERENCE: 38417-1312
; CURRENT APPLICATION NUMBER: US/10/097,554A
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: 60/275,266
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1032
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE: 5
; NAME/KEY: CDS
; LOCATION: (1)...(1032)
; OTHER INFORMATION: nucleotide sequence encoding Cre recombinase
US-10-097-554A-5

Query Match 58.8%; Score 617.4; DB 13; Length 1032;
Best Local Similarity 75.1%; Pred. No. 8.6e-127;
Matches 771; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

QY 23 TGAGCAACCTGCTGACCGTGCACCAAGAACCTGCCCGCCCTGCGCGTGGAGCGCCACGCG 82

Db	2	TGTC	CAATTT	TA	CTG	ACCG	TA	CA	CAAA	ATTT	GC	CTG	CA	TTT	AC	CGG	TC	GA	CA	AC	GA	GTG	61
Qy	83	AC	GAG	GT	TC	GC	CA	GA	AA	CT	GA	TG	GA	CA	TG	TT	CC	GC	CA	CG	CG	CA	142
Db	62	AT	GAG	TT	CG	CA	GA	AA	CT	GA	TG	GA	CA	TG	TT	CA	GG	GA	TC	GC	CA	GG	121
Qy	143	CT	GA	GA	AT	GC	TG	CT	GA	GC	TG	TC	CG	CA	GC	TC	GG	CG	CG	CT	GT	GA	202
Db	122	CT	GA	AA	AT	CT	TT	CG	TT	TC	CG	TT	TC	CG	GT	TC	GG	CG	CA	TG	GA	TT	181
Qy	203	GA	AG	TG	GT	CC	CG	CG	CA	GC	CG	AG	CA	CT	GG	CG	CA	CT	GG	CG	CA	CT	262
Db	182	GA	AA	TG	GT	TC	CG	CG	CA	GC	CT	GA	AG	AT	TC	CG	CA	AT	TC	CG	CA	AT	241
Qy	263	GC	GC	CT	GG	CG	TC	GA	GA	CA	CT	CA	GA	CA	CT	GG	CG	CA	CT	GG	CG	CA	322
Db	242	GC	GT	TC	GG	CAG	TAA	AA	CT	AT	CG	CA	CA	CT	TC	GG	CG	CA	CT	TC	GG	CG	301
Qy	323	GA	CG	GG	CT	CG	CG	CG	CG	CG	CA	CA	CG	CG	TC	GG	CG	CA	CG	TC	GG	CG	382
Db	302	GG	T	CC	GG	CT	GC	CA	CA	GA	TG	CA	CA	CT	TC	GG	CG	CA	CT	TC	GG	CG	361
Qy	383	GA	AG	GA	AA	CG	TG	GA	CG	CG	CG	CG	CG	CA	CG	CG	CG	CG	CG	CG	CG	CG	442
Db	362	GA	AA	GA	AA	CG	TT	GA	TC	CG	CG	TC	GA	CG	TC	GA	CG	TC	GA	CG	TC	GA	421
Qy	443	AC	TT	TC	GA	CC	AG	GT	CG	CA	CG	CT	GA	TG	GA	GA	CA	CG	CA	CG	CT	GA	502
Db	422	AT	TT	TC	GA	CC	AG	TT	CG	TT	CA	CT	CA	TG	GA	AA	TA	GG	AT	CG	CA	TA	481
Qy	503	TG	GC	TT	TC	TG	GG	CA	T	CG	CT	TA	CA	CA	CC	TC	GG	CG	AT	CG	CG	CG	562
Db	482	TG	GC	AT	TT	TC	GG	GA	TT	CG	TT	TA	TA	CA	CC	TC	GG	CG	AT	CG	CG	CG	541
Qy	563	GC	GT	GA	AG	GA	CA	T	CA	CG	CA	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	622
Db	542	GG	GT	TA	AG	GA	TA	T	CA	CG	TA	CT	GA	CG	GT	GA	GA	AT	GT	TA	AT	CC	601
Qy	623	AG	AC	CT	TG	GT	GA	CA	CG	CG	CG	TC	GG	GA	AG	CG	CT	GA	CG	CT	GG	CG	682
Db	602	AA	AC	GT	TG	TT	AG	CA	CG	CA	GG	GT	GA	GA	AG	CA	CT	TA	GG	CG	TA	CT	661
Qy	683	TG	GA	CG	CT	GG	AT	CA	CG	TC	GA	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	742
Db	662	TC	GA	CG	AT	GG	AT	TC	CG	TC	TC	GG	TC	GA	TC	GA	TC	CG	AA	TA	CT	AC	721
Qy	743	GC	GT	CG	CA	GA	AC	GG	CG	TG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	802
Db	722	GG	GT	CA	GA	AA	AA	TG	GT	TC	CG	CG	CG	CA	TC	GC	CA	CG	CG	CA	CT	TA	781
Qy	803	TG	GA	GG	CA	CT	TC	GA	GG	CA	CC	CA	CG	CG	CT	GA	TC	AC	GG	CG	CA	GG	862
Db	782	TG	GA	AG	GA	TT	TT	GA	AG	CA	CT	CA	TC	GA	TT	TA	CG	GG	CG	TC			

RESULT 9

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US-10-161-403-58
; Sequence 58, Application US/10161403
; Publication No. US2003019104A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Sheilard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 1032
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1032)
; OTHER INFORMATION: nucleotide sequence encoding
US-10-161-403-58

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Query Match	58.8%	Score 617.4	DB 15	Length 1032
Best local Similarity	75.1%	Pred. No. 8.6e-127		
Matches	771	Conservative 0	Mismatches 256	Indels 0
QY	23	TGAGCAACCTGCTGACCGTCACACAGAACCTGCCCGCCTGCCCGTGGACGCCACCGACGG	82	
Db	2	TGTCCAATTTACTGACCGTACACCAAAATTTGCCTGCATTACCGGTGCATGCAACGATG	61	
QY	83	ACGAGGTGCGCAAGAAACCTGATGACATGTTCCGCGACCGCCAGGCCTTTCAGCGAGCACA	142	
Db	62	ATGAGGTTTCGAAAGAACCTGATGACATGTTCAGGATCGCCAGGCGTTTCTGAGCAT	121	
QY	143	CCTGGAAGATGCTGCTGACGCGTGC CGCGAGCTGGCGCGCTGGTCAAGCTGAACAACC	202	
Db	122	CCTGGAATAATGCTTCTGTCTGCTTTCGCGTTCGCGGTCGTTGGCGGCGATGGTGAAGTTGAATAACC	181	
QY	203	GCAAGTGGTTCCCGCGACCGAGGACCTGGCGGACTACCTGCTGTACTCTGCAGAGCC	262	
Db	182	GGAAATGGTTTCCCGCAGAACCTGAGATGTTTGGCGATTCTTCTATATCTTCAGGCGC	241	
QY	263	CGCGCTTGGCCGTGGAAGACCATCAAGCAGACCTTGGGCCAGCTGAAACATGCTGCACGCC	322	
Db	242	CGCGTCTGGCAGTAAACAACTATCGACCAACATTTGGGCCAGCTAAACATGCTTCATCGTC	301	
QY	323	GCACGCGCTCGCCCGCCACGCGACGACGACGCGCGCTGGTGGTATGGCGCGCATCC	382	
Db	302	GGTCCGGCTGCCACGACCAAGTGACAGCAATGCTGTTTCACTGGTTATGGCGCGGATCC	361	
QY	383	GCAAAGAGAACGTGGACCGCGCGGACCGCCCAAGCAGAGGCCTTGGCTTCGAGCGCACCG	442	
Db	362	GAAGAAGAACGTTGATGCGGTTGACCTGCAAAACAGGCTCTAGCGTTGGAACGCACTG	421	
QY	443	ACTTCGACCAAGTGGCAGCGCTGATGAGAAACAGCGACCGCTGCCAGGACATCCGCAACC	502	
Db	422	ATTTTCAGCAGGTTCTGTTCACTCATGGAAATAGCGATCGCTGCCAGATATACGTAACT	481	
QY	503	TGSCCTTCTTGGGCATCGCTCAACACCTGCTGCGCATCGCGGAGATCGCCCGCATCC	562	
Db	482	TGSCATTTCTGGGGATGCTCTTATTAACACCTGTTACGTATAGCGGAAATTCGAGGATCA	541	
QY	563	GCCTGAAGGACATCAAGCCGACCGCGGCGCGCATGCTGATCCATCGCGCGCACCA	622	

Db 542 GGGTTAAAGATATCTCAGTACTACGGTGGGAGAAATGTTAAATCCATATTGGCAGAACGA 601
Qy 623 AGACCTTGGTGAAGACCGCGCGCTGGAGAGGCGCTGAGCCTGGGCGTGACCAAGCTGG 682
Db 602 AAACGCTGGTTAGACCGCAGGTGTAGAGAGGCACCTTAGCCTGGGGGTACTAACTGG 661
Qy 683 TGGAGCGCTGGATCAGCGTGAAGCGCGTGGCCGACGACCCCAACAACACTACTGTTTGGC 742
Db 662 TCGAGCGATGATTTCCGTCCTCTGCTGTAGCTGATGATCCGAATAACTACTGTTTGGC 721
Qy 743 GCGTGGCAGAAACGGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 802
Db 722 GGGTCAGAAAATAATGGTGTGGCGCGCATCTGCCACCGACGACGCTATCAACTCGCGCCC 781
Qy 803 TGGAGGCGATCTTCAGGCGCACCCACCGCTGATCTACGGCGCGCAAGGACGACAGCGGCC 862
Db 782 TGGAGGAGATTTTGAAGCACTCATCGATTGATTACGGCGCTTGAAGTACTCTGTC 841
Qy 863 AGCCTTACCTGGCTGAGCGGCGCACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 922
Db 842 AGAGTACCTGGCGCTGCTGGACACAGTGGCGCGCTGCGAGCGCGCGGAGATATGGCC 901
Qy 923 GCGCGCGCTGAGATCCCGAGATCATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGC 982
Db 902 GCGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGGTGGCTGGACCAATGTAAATATG 961
Qy 983 TGATGAACCTACATCCGCAACCTGACAGCGAGACCGCGCGCGCGCTGACCAACGTGAACATG 1042
Db 962 TCATGAACCTATATCCGTAACCTGATAGTAAGGAGGCAATGGTGGCGCTGCTGGAAG 1021
Qy 1043 ACGCGCA 1049
Db 1022 ATGGCGA 1028

RESULT 10

US-09-853-033-3
; Sequence 3, Application US/09853033
; Patent No. US20020100068A1
; GENERAL INFORMATION:
; APPLICANT: CHAMBON, PIERRE
; APPLICANT: METZGER, DANIEL
; TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION
; FILE OF INVENTION: MEDIATED BY MODIFIED CRE-ER
; FILE REFERENCE: 065691/0222
; CURRENT APPLICATION NUMBER: US/09/853.033
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: FR 00/12570
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1983
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1983)
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric sequence
; OTHER INFORMATION: Homosapiens-Bacteriophage P1

Query Match 58.8%; Score 617.4; DB 10; Length 1983;
Best Local Similarity 75.1%; Pred. No. 8.3e-127;
Matches 771; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

Qy 23 TGACCAACTGCTGACCGTGACCAAGACCTGCGCGCGCGCTGCCCGTGAGCGCCACCGCG 82
Db 2 TGTCCAAATTTACTGACCGTGACCAAAATTTGCGCTGATACCGGTGATGAGTCAACGAGTG 61
Qy 83 ACGAGGTGCGCAAGAACCTGATGACATGTTCCGCGACCGCGCGCGCTTACGCGAGCACA 142

Db 62 ATGAGGTTCCAAAGAACCTGTAGTGAATGTTTCTAGGAGATCGCCAGGCGTCTTTCTGAGCAT 121
Qy 143 CTGGAAGATGCTGCTGAGCGTGTGCGCAGCTGGGCGCGCTGCTGCTCAAGCTGAAACAAC 202
Db 122 CTTGGAATATGCTTCTGTCGCTTGGCGGTGCTGGGCGGCAATGTCGAAGTTGAAATAAC 181
Qy 203 GCAAGTGGTTCCCGCGCGAGCCGAGGAGTGTGCGGACTTACCTGTGTACTCTGACGGCCC 262
Db 182 GGAATATGGTTTCCCGCAGAACCTGGAAGATGTTCCGGAATATCTTCTATATCTTCTCAGCGC 241
Qy 263 GCGGCTGCGCGGTGAAGACCATCCAGCAGCAGCTGGGCGAGCTGAACATGCTGCACCGCC 322
Db 242 GCGGCTGCGCAGTAATAAATCTATCCAGCAATTTGGGCCAGCTAAACATGCTTCTCATCGTC 301
Qy 323 GCAGCGGCTGCGCGCGCGCGCGAGCAGCAACCGCGTGGAGCTGTGATGCGCGCGCATCC 382
Db 302 GGTCCGGGCTGCCACGACCAAGTGACAGCAATGCTGTTTCACTGGTTATGCGCGGATCC 361
Qy 383 GCAAGGAGAACTGTGAGCGCGCGAGCGCGCAAGCAGCGCTTGGGCTTGGAGCGCAACG 442
Db 362 GAAAGAGAAACGTTGATGCGGTTGAACGTCGCAAAACAGGCTCTAGCGGTTTGAACGCACTG 421
Qy 443 ACTTCCAGCAGGTGCGCAGCTGATGAGAGAACAGCAGCAGCTGCGCAGGACATCCGCAAC 502
Db 422 ATTTCCAGCAGGTGCTGCTCATCTATGAAATAGCGATCGCTGCCAGGATATACGTAATC 481
Qy 503 TGGCCTTCTTGGGCTATCGCCTACAAACCGCTGTGCGCATCGCCGAGATCGCCCGCATCC 562
Db 482 TGGCAATTTCTGGGATTGCTTATAACACCGCTGTACGTATAGCCGAATTTGCCAGGATCA 541
Qy 563 GCGTGAAGACATCAGCGCGCACCGAGCGCGCGCATGCTGATGCCATCGCGCGCGCAACCA 622
Db 542 GGGTTAAAGATATCTCACGTAAGCTGAGCGTGGGAGAAATGTTAATCCATTTTGGCAGAACGA 601
Qy 623 AGACCTGCTGAGCACCGCGCGTGGAGAGCGCCTGAGCGCTGGCGGTGACCAAGCTGG 682
Db 602 AAACGCTGGTTAGCACCGCGAGGTGTAGAGAGGCACTTAGCCTGGGGGTAACTAAACTGG 661
Qy 683 TGGAGCGCTGGATCAGCGTGGCGGCTGGCGCGACGACCCCAACAACTACTCTGTTCTGCC 742
Db 662 TCGAGCGATGGATTTCCGCTCTGCTGTAGCTGATGATCGAATACTACTCTGTTTGGC 721
Qy 743 GCGTGGCAAGAACGGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 802
Db 722 GGGTCAGAAAAAATGGTGTGGCGCGCATCTGCCACAGCCAGCTATCAACTCGCGCCC 781
Qy 803 TGGAGGCGATCTTTCGAGGGCCACCCACCGCTGATCTACGCGCGCAAGGAGCAGCGGCC 862
Db 782 TGGAGGGATTTTGAAGCAACTCATCGATTGATTACGCGCTAAGGATGACTCTGGTC 841
Qy 863 AGCGCTACCTGGGCTTGGAGCGCGCACAGCGCGCGCGCGCGCGCGCGCGCGCGCGC 922
Db 842 AGAGATACCTGGGCTGCTGGACACAGTGGCGCGTGTGCGAGCGCGCGGAGATATGGCCC 901
Qy 923 GCGCGCGGTGAGCATCCCGAGATCATGAGCGCGCGCGCGCTGGACCAAGCTGAACATCG 982
Db 902 GCGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGGTGGCTGGACCAATGTAAATATG 961
Qy 983 TGATGAACCTACATCCCAACCTGAGCAGCGAGACCGCGCGCATGTTGGCGCTCTCGAGG 1042
Db 962 TCATGAACCTATATCCGTAACCTGATAGTAAGGAGGCAATGGTGGCGCTGCTGGAAG 1021
Qy 1043 ACGCGCA 1049
Db 1022 ATGGCGA 1028

RESULT 11
US-09-853-033-5
; Sequence 5, Application US/09853033
; Patent No. US20020100068A1
; GENERAL INFORMATION:
; APPLICANT: CHAMBON, PIERRE

Db 242 GGGGCTGGCAGTAAAAATATCCAGCAACATTTGGGCCAGCTAAACATGCTTCATCGTC 301
QY 323 GCAGGGCTGCGCCCGCCAGCAGCAAGCCGCTGAGCCTGTGTGATGCGCCGCATCC 382
Db 302 GGTCCGGGCTGCCAGCAAGTGACAGCAATGCTTCACTGGTTATGCGCGGATCC 361
QY 383 GCAAGGAGAACGTGACGCGCGGAGCGCCAGCAGGCGCTGCGCTTCGAGCGCAGC 442
Db 362 GAAAGAAACGTTGATGCGCGTGAAACGTCGCAACAGGCTCTAGCGTTGCAACGCACTG 421
QY 443 ACTTCGACAGGTGGCGCAGCTGATGGAGAACAGCAGCGCTGCCAGGACATCCGCAACC 502
Db 422 ATTTGACACAGTTCGTTCACTCATGGAATAAGCATGCTGCCAGGATATACGTAATC 481
QY 503 TGGCTTCCTGGGCAATCGCTCAACACCTCTGCGCATCGCCGAGATGCGCCGCATCC 562
Db 482 TGGCAATTTCTGGGATTTGTTATAACACCTCTAGTATAGCCGAAATGCGCAGGATCA 541
QY 563 GGTGAAGGACATCAGCGCACGAGCGGCGCGCATGCTGATCCACATCGCGCGACCA 622
Db 542 GGGTTAAAGATATCTCAGCTACTGACGCTGGGAGAAATGTTATCCATATGCGCAGACGA 601
QY 623 AGACCTGTGTAGCAGCCGCGCTGGAGAGCGCCCTGAGCCTGGGCGTGACCAAGCTGG 682
Db 602 AAACGCTGTTAGCACCGCAGGCTGAGAGAGGCACTTAGCCTGGGGTAACTAAACTGG 661
QY 683 TGGAGCGTGGATCAGCGGTGAGCGCGGTGGCGACGACCCCAACAACTACCTGTTCTGCC 742
Db 662 TCGAGCGATGGATTTCCGCTCTCTGGTGTAGCTGATGATCCGAAATAACTACCTGTTTGGC 721
QY 743 GGTGCGCAAGAACGCGTGGCGCCCGCCAGCGCCACAGCAGCTGAGCAGCCCGGGCCC 802
Db 722 GGGTCAGAAAAAATGGTGTGCGCGCCCATCTGCCACCAGCAGCATCAACTCGCGGCC 781
QY 803 TGGAGGGATCTTCAGAGCCACCCACCGCTGATCTAGCGGCCAAGGACGACACGCGCC 862
Db 782 TGGAGGATTTTGAAGCACTCATCGATTGATTTACGGCGCTAAGGATGACTCTGGTC 841
QY 863 AGCGCTACCTGGCTGGAGCGCCACAGCGCGCGCGTGGCGCCCGCCGACATGCGCCC 922
Db 842 AGAGATACCTGGCTGGTCTGGACACAGTGCCCGCTGCGAGCGCGGAGATGCGCCC 901
QY 923 GCGCGCGGTGAGCATCCCGAGATCATGAGCGCGCGCGGTGAGCAACGCTGAACATCG 982
Db 902 GCGCTGGAGTTTCAATACCGGAGATCATGCAAGCTGGTGGCTGGACCAATGTAATATTG 961
QY 983 TGATGAATACATCCGCAACCTGGAGCAGCGAGCCGCGCCATGCTGCGCTGCTGGAGG 1042
Db 962 TCATGAATATATCCGTAACTGGATAGTGAACAGGGGCAATGGTGGCGCTGCTGGAG 1021
QY 1043 ACGGCGA 1049
Db 1022 ATGGCGA 1028

RESULT 13
US-10-353-445-4
; Sequence 4, Application US/10353445
; Publication No. US20030119166A1
; GENERAL INFORMATION:
; APPLICANT: Baszczynski, Christopher L.
; APPLICANT: Lyszniak, Leszek A.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Guan, Xueni
; APPLICANT: Rao, Guru
; APPLICANT: Tagliani, Laura A.
; TITLE OF INVENTION: A No. US20030119166A1 Method For The Integration Of Foreign DNA
; FILE REFERENCE: 5718-66 (amended listing)
; CURRENT APPLICATION NUMBER: US/10/353,445
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US/09/193,503B

; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Nucleotide
; OTHER INFORMATION: sequence encoding a Cre:FLPm polypeptide, Cre
; OTHER INFORMATION: from Bacteriophage P1 and FLP (Maize preferred
; OTHER INFORMATION: codons) from Saccharomyces
US-10-353-445-4

Query Match 58.8%; Score 617.4; DB 15; Length 2346;
Best Local Similarity 75.1%; Pred. No. 8.2e-127;
Matches 771; Conservative 0; Mismatches 256; Indels 0; Gaps 0;
QY 23 TGAGCAACCTGCTGACCGTGCCAGAACCTGCGCCGCTGCCGTGGAGCCACGACG 82
Db 2 TGGCCAAATTTACTACCGGTACACCAAAATTTGCCCTGCAATTACCGGTGCAATGCAACGAGTG 61
QY 83 ACAGAGGTGCGCAAGAACCTGATGACATGTTCCGCGACCGCCAGCGCTTCAGCGAGCACA 142
Db 62 ATGAGGTTGCGAAGAACCTGATGACATGTTGAGGATCGCCAGCGGTTTCTGAGCAT 121
QY 143 CCTGGAAGATGCTCTGAGCGTGTGCCGAGCTGGCGCGCTGGTGTGCAAGCTGAACAACC 202
Db 122 CCGCAAAATGCTTCTGTCGTTGCGCGTCTGGCGGCATGTTGCAAGTTGAATAACC 181
QY 203 GCAAGTGGTTCCTCCCGCAGCGCCGAGGACGTGCGGACTACCTGCTGTACTGCGAGGCC 262
Db 182 GGAAATGGTTTCCGCGAGAACCTGAAGATGTTCCGATTAATCTTCTATATCTTCAGGGCG 241
QY 263 GCGGCTGGCGCTGAAGACCATCCAGCAGCATCTGGCGCGCTGGTGTGCAAGCTGCAACGCC 322
Db 242 GCGGTCTGGCAGTAAACAACTATCCAGCAACATTTGGGCGCAGCTAAACATGCTTCATCGTC 301
QY 323 GCAGCGGCTGCCCCCGCCAGCGACAGCAACGCGCTGGAGCCTGGTGTGATGCGCGCATCC 382
Db 302 GGTCCGGCTGCCACGACCAAGTGACAGCAATGCTGTTCACTGTTTATGCGGCGGATCC 361
QY 383 GCAAGGAGAACGTGAGCGCGCGGAGCGCGCAAGAGGCGCTGGCCTTCGAGCGCACCG 442
Db 362 GAAAGAAACGTTGATGCGCGTGAAACGTCGCAACAGGCTCTAGCGTTGCAACGCACTG 421
QY 443 ACTTCGACAGGTGGCGCAGCTGATGGAGAACAGCAGCGCTGCCAGGACATCCGCAACC 502
Db 422 ATTTGACACAGTTCGTTCACTCATGGAATAAGCATGCTGCCAGGATATACGTAATC 481
QY 503 TGGCCTTCCTGGGCAATCGCTCAACACCTCTGCGCATCGCCGAGATGCGCCGCATCC 562
Db 482 TGGCAATTTCTGGGATTTGTTATAACACCTCTAGTATAGCCGAAATGCGCAGGATCA 541
QY 563 GCGTGAAGGACATCAGCGCGCACGAGCGGCGCGCATGCTGATCCACATCGCGCGACCA 622
Db 542 GGGTTAAAGATATCTCAGCTACTGACGCTGGGAGAAATGTTATCCATATGCGCAGACGA 601
QY 623 AGACCTGTGTAGCAGCCGCGCTGGAGAGCGCCCTGAGCCTGGGCGTGACCAAGCTGG 682
Db 602 AAACGCTGTTAGCACCGCAGGCTGAGAGAGGCACTTAGCCTGGGGTAACTAAACTGG 661
QY 683 TGGAGCGCTGGATCAGCGGTGAGCGCGGTGGCGACGACCCCAACAACTACCTGTTCTGCC 742
Db 662 TCGAGCGATGGATTTCCGCTCTCTGGTGTAGCTGATGATCCGAAATAACTACCTGTTTGGC 721
QY 743 GGTGCGCAAGAACGCGTGGCGCCCGCCAGCGCCACAGCAGCTGAGCAGCCCGGGCCC 802

Db 722 GGGTCAGAAAAATGGTGTTCGGCGCCATCTGCCACAGCCAGCTATCAACTCGCGCCC 781
Qy 803 TGGAGGGATCTTCGAGGGCACCCCGCTGATCTACCGGCGCAAGGACGACGCGCC 862
Db 782 TGGAAAGGATTTTGAAGCAACTCATCGATTGATTTACGGCGCTAAGGATGACTCTGCTC 841
Qy 863 AGCGCTACCTGGCGTGGAGCGCCACAGCGCCGCGGTGGCGCGCCCGCGACATGGCCC 922
Db 842 AGAGATACCTGGCTGGTCTGACACAGTGCCTGGTTCGGAGCGCGCGAGATATGGCCC 901
Qy 923 GCGCGCGGTGAGCATCCCCAGATCATGACGCGCGCGCTGGACCAACGTTGAACATCG 982
Db 902 GCGCTGGAGTTTCAATACCGAGATCATGCAAGCTGGTGGCTGGACCAATGTAATATTG 961
Qy 983 TGATGAATACATCCGAACTCTGGACAGGACCGCGGCCCATGTTGGCGCTCTGCTGGAGG 1042
Db 962 TCATGAATATATCCGTAACTTGGATAGTGAACAGGGGCAATGGTGGCGCTGCTGGAAG 1021
Qy 1043 ACGCGCA 1049
Db 1022 ATGGCGA 1028

RESULT 14

US-10-353-445-7
; Sequence 7, Application US/10353445
; Publication No. US20030119166A1
; GENERAL INFORMATION:
; APPLICANT: Baszczynski, Christopher L.
; APPLICANT: Lyznik, Leszek A.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Guan, Xueni
; APPLICANT: Rao, Guru
; APPLICANT: Tagliani, Laura A.
; TITLE OF INVENTION: A No. US20030119166A1 Method For The Integration Of Foreign DNA
; FILE REFERENCE: 5718-66 (amended listing)
; CURRENT APPLICATION NUMBER: US/10/353,445
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US/09/193,503B
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence
; OTHER INFORMATION: encoding a Cre:FLP polypeptide, Cre from
; OTHER INFORMATION: Bacteriophage P1 and FLP from Saccharomyces
US-10-353-445-7

Query Match 58.8%; Score 617.4; DB 15; Length 2346;
Best Local Similarity 75.1%; Pred. No. 8.2e-127;
Matches 771; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

Qy 23 TGAGCAACCTGCTGACCGTGCACAGAACCTCGCGCCCTCGCGTGGAGCCACCGCG 82
Db 2 TGGCCAATTTACTGACCGTACACCAAAATTTGCTGATACCGGTGATGCAACAGATG 61
Qy 83 ACGAGGTGCGCAAGAACTGATGACATGTTTCCGCGACCGCGACGCTTCAGCGAGACA 142
Db 62 ATGAGGTGCGCAAGAACTGATGACATGTTTCCGCGACCGCGACGCTTCAGGATA 121
Qy 143 CCTGGAAGATGCTGCTGAGCGGTGTGCGCAGCTGGCGCGCTGGTGAAGTGAACACC 202

RESULT 15

US-10-353-445-8
; Sequence 8, Application US/10353445
; Publication No. US20030119166A1
; GENERAL INFORMATION:
; APPLICANT: Baszczynski, Christopher L.
; APPLICANT: Lyznik, Leszek A.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Guan, Xueni

Db 122 CCTGAAAAATGCTTCTGTCCGTTTCGGCGCGCATGGTGCAGTTGAATAACC 181
Qy 203 GCAAGTGTTCCTCCCGCGAGCCCGAGGACGTGCGGAGCTTACCTGTGTACCTGCGAGGCC 262
Db 182 GGAATGTTTCCCGCGAGAACTTGAAGATGTTCCGATTAATCTTATATCTTCAGGCGC 241
Qy 263 GCGGCTGCGCGTGAAGACCATCCAGCAGCACTTGGCCAGCTGAACATGTGTCACTGC 322
Db 242 GCGGCTGCGCAGTAAAAACTATCCAGCAACATTTGGGCCAGCTAAACATGCTTCATGTC 301
Qy 323 GCAGCGGCTGCGCGCGCGCGCGAGCAGCAGCGCGCTGAGCTGTGTGATGGCGCCGATCC 382
Db 302 GGTCCGGGCTGCCAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 361
Qy 383 GCAAGGAAACGTGAGCGCGCGCGCGCGAGCGCGCGCGCTGAGCGCGCTGAGCGCGCGCG 442
Db 362 GAAAGAAAAGTGTGATGCGCGGTGAACGTGCAAAACAGGCTCTAGCGTTCGAACGCACTG 421
Qy 443 ACTTCGACAGGTGCGCAGCGCTGATGGAGAACAGCAGCGCGCTGCCAGACATCCGCAACC 502
Db 422 ATTTTCGACAGGTTCGTTCACTCATGGAATAATAGCATCGCTGCCAGGATATACGTAATC 481
Qy 503 TGGCTTCCTGGGCTGCGCTTACACACCTGCTGCGCATCGCGATCGCGAGATCCCGCGATCC 562
Db 482 TGGCATTTCTGGGATTTCTTATAACACCTGTTACGTATAGCCGAAATTCGACGATCA 541
Qy 563 CGGTGAAGGACATCAGCGCGCACCGCGCGCGCGCATGCTGATCCACATCCGCGCGCACCA 622
Db 542 GGGTTAAAGATATCTCAGTACTGACGCTGGAGAAATGTTAATCCATATTTGGAGAAAGA 601
Qy 623 AGACCTGTTGAGACCGCGCGCGCGCTGAGAGAGCGCTGAGCTGGCGGTGACCAAGCTGG 682
Db 602 AAACGCTGGTTAGCACCGCAGGTGTAGAGAAAGGCACTTAGCTGGGGTAACTAACTGG 661
Qy 683 TGGAGCGCTGATCAGGTGAGCGCGCTGGCGGACGACCCCAACAACTACCTGTTCTGCC 742
Db 662 TCGAGCGATGGATTTCCGTCTCTGCTGTAGTGTATGATCCGATAAATACTACCTGTTTGGC 721
Qy 743 CGGTGCGCAAGAACGGGTGCG 802
Db 722 GGGTCAGAAAAATGGTGTTCGGCGCGCACTGCGCACGACGACTATCAACTCGCGCGCC 781
Qy 803 TGGAGGCGATCTTCAGGCGCACCCACCGCTGATCTACGGCGCGCAAGGACGACAGCGCGC 862
Db 782 TGGAAAGGATTTTGAAGCAACTCATCGATTGATTACGGCGCTAAGATGACTCTGGTC 841
Qy 863 AGCGCTACCTGGCGTGGAGCGCGCACAGCGCGCGCGCTGGCGCGCGCGCGCGCGCGCGCG 922
Db 842 AGAGATACCTGGCGTGGTCTGAGCACAGTGCCTGTCGAGCGCGCGCGCGCGCGCGCGCG 901
Qy 923 GCGCGCGGTGAGCATCCCGAGATCATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 982
Db 902 GCGCTGGAGTTTCAATACCGAGATCATGCAAGCTGGTGGCTGAGCAATGTAATATTG 961
Qy 983 TGATGAATACATCCGCAACCTGGAACAGCGAGACCGCGCGCATGTTGTCGCTGCTGGAGG 1042
Db 962 TCATGAATATATCCGTAACTTGGATAGTGAACAGGGGCAATGGTGGCGCTGCTGGAAG 1021
Qy 1043 ACGCGCA 1049
Db 1022 ATGGCGA 1028

APPLICANT: Rao, Guru
APPLICANT: Tagliani, Laura A.
TITLE OF INVENTION: A No. US20030119166A1el Method For The Integration Of Foreign DNA
TITLE OF INVENTION: Eukaryotic Genomes
FILE REFERENCE: 5718-66 (amended listing)
CURRENT APPLICATION NUMBER: US/10/353,445
CURRENT FILING DATE: 2003-01-29
PRIOR APPLICATION NUMBER: US/09/193,503B
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/099,435
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: 60/056,627
PRIOR FILING DATE: 1997-11-18
PRIOR APPLICATION NUMBER: 60/065,613
PRIOR FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 2346
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Sequence
OTHER INFORMATION: encoding a FLPm:Cre polypeptide, FLP from
OTHER INFORMATION: Saccharomyces (maize preferred codons), and Cre
OTHER INFORMATION: from Bacteriophage P1
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(2346)
US-10-353-445-8

Query Match 58.8%; Score 617.4; DB 15; Length 2346;
Best Local Similarity 75.1%; Pred. No. 8.2e-127;
Matches 771; Conservative 0; Mismatches 256; Indels 0; Gaps 0;
Qy 23 TGAGCAACCTGCTACCGTGCACAGAACCTGCCGCGCCCTGCCGTGGAGCCACCAGCG 82
Db 1316 TGGCCATTACTGACCGTACACCAAAATTTGCCCTGCATTACCGTGCATGCAACAGAGTG 1375
Qy 83 ACGAGGTGCGAAGAACCTGATGACATGTTCCGCGACCGCCAGGCGCTTCAGCGAGCACA 142
Db 1376 ATGAGTTGCGAAGAACCTGATGACATGTTTCAGGATCGCCAGCGGTTTCTGAGCATA 1435
Qy 143 CCTGGAAGATGCTGCTGAGCGTGTGCCAGCTGGCGCGCTGGTGCAGCTGAACAC 202
Db 1436 CCTGGAAAATGCTTCTGTCCTGTTGCCGTTCTGGCGGCGATGGTCAAGTTGAATAAC 1495
Qy 203 GCAAGTGGTTCGCCCGCGAGCGCGAGGACGTGCGGACTACCTGCTGTACCTGCAGGCCC 262
Db 1496 GGAATGGTTTCCGCGAGAACTGAAGATGTTCCGGATTATCTTCTATATCTCAGGCGC 1555
Qy 263 CGGCGCTGGCGTGAAGAACCTCAGCAGACCTGGGCGAGCTGAAACATGCTGCACCGCC 322
Db 1556 CGGCTCTGGCAGTAAAAAATAATCCAGCAACATTTGGGCGAGCTAAACATGCTTCATCGTC 1615
Qy 323 GCAGGCGCTGCCCGCCCGCGAGCGCGACGACGCGGCTGAGCTGGTGCATGGCGCATCC 382
Db 1616 GGTCCGGCTGCCACGACCAAGTACAGCAATGCTGTTCTACTGTTATGGCGGATCC 1675
Qy 383 GCAAGGAGAACGTTGAGACCGCGCGAGCGCGCAAGAGCGCCCTGGCCTTCGAGCGCACCG 442
Db 1676 GAAAGAAACGTTGATGCCCGGTGAACGTGCAAAACAGGCTCTAGCGTTGCAACGCACTG 1735
Qy 443 ACTTCGACCGGTGCGAGCTGATGAGAGACAGCGACCGCTGCCAGGACATCCGCAACC 502
Db 1736 ATTTTCGACCGAGTTTCGTTCACTCATGGAATAAGCATCGCTGCCAGGATATACGTAATC 1795
Qy 503 TGGCCTTCCTGGGATCGCCTACAAACACCTGCTGGCATCGCCGAGATGCGCCGCGATCC 562
Db 1796 TGGCATTTCTGGGATGCTTTATAACACCTGTTACGCTATAGCCGAAATTCGCGAGATCA 1855
Qy 563 GCGTGAAGGACATCAGCGCGACCGCGCGCGCATGCTGATCCATCGCGCGCACCA 622

Db 1856 GGGTTAAAGATATCTACGTACTGACGGTGGGAGAAATGTTAAATCCATATTGGGAGAACGA 1915
Qy 623 AGACCCCTGGTGAAGCACCGCGCGGTGGAGAAAGCCCTGAGCCTGGGCGGTGACCAAGCTGG 682
Db 1916 AAACGCTGGTTAGCACCGCAGGTGTAGAGAAAGGCACTTAGCTGGGGGTAACTAAACTGG 1975
Qy 683 TGGAGCGCTGATCAGCGTGAAGCGGTGGCCGAGACCCGCAACAACTACTGTTCTGTC 742
Db 1976 TCGAGCGATGGAATTTCCGCTCTCTGGTGTAGCTGATGATCCGAATAACTACTGTTTGGCC 2035
Qy 743 GCGTGCCTCAAGAACCGGCTGGCGCCCGCCAGCGCCACAGCCAGCTGAGCACCGCGGCC 802
Db 2036 GGGTCAGAAAAAATGTTGTTGCCGCGCATCTGCCACAGCCAGCTATCAACTGCGGCC 2095
Qy 803 TGGAGGCGCATCTTTCGAGGCCACCCAGCCGCTGATCTACGGCGGCAAGAGACGACGCGGCC 862
Db 2096 TGGAAAGGATTTTGAAGCAACTCATCGATTGATTTACGGCGCTAAGGATGACTCTGTC 2155
Qy 863 AGCGCTACCTGGCTGGAGCGGCCACAGCGCCCGCGTGGGCGCGCCGCGGACATGGCCC 922
Db 2156 AGAGATACCTGGCTGGTCTGGACACAGTCCCGTGTCCGAGCGCGCGAGATATGGCCC 2215
Qy 923 GCGCGCGCGTGAAGCATCCCGAGATCATGAGCGCGCGCTGACCAACAGTGAACATCG 982
Db 2216 GCGCTGAGTTTCAATACCGAGATCATGCAAGCTGGTGGCTGGACCAATGTAATATTG 2275
Qy 983 TGATGAACATCATCCGCAACTGGACAGCGGCGGCGGCGGCTGCTGCTGCGAGG 1042
Db 2276 TCATGAACATATCCGTAACCTGGATAGTAGTGAACAGGGGCAATGGTGGCGCTGCTGGAAG 2335
Qy 1043 ACGCGCA 1049
Db 2336 ATGGCGA 2342

Search completed: December 16, 2003, 05:43:24
Job time : 1949 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 16, 2003, 01:24:58 ; Search time 2664 Seconds
(without alignments)
9579.467 Million cell updates/sec

Title: US-09-662-128A-1

Perfect score: 1050

Sequence: 1 atgcccaagaagaaggaa.....gocgtggaggagggcgac 1050

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum-DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	390	37.1	688	12	BI651236	BI651236 603298328
2	231	22.0	431	9	AW211323	AW211323 uo79f01.y
3	181.2	17.3	563	12	BI650191	BI650191 603296283
4	158.8	15.1	340	9	AW212478	AW212478 uo89c03.x

C	5	150.6	14.3	338	9	AW211972	AW211972 uo79f01.x
	6	128.2	12.2	343	9	AW210918	AW210918 uo89c09.y
	7	86	8.2	836	12	BI556329	BI556329 603237448
C	8	84.4	8.0	822	29	CC405275	CC405275 PUHJX22TD
C	9	81.8	7.8	838	29	BZ728954	BZ728954 OGBDN92TM
	10	79.8	7.6	288	29	FR0013439	FR0013439 F.rubripe
C	11	75.6	7.2	925	29	CNS0091P	AL004689 Drosophil
	12	74.6	7.1	727	13	BQ483660	AL053012 WHB3511.B
	13	74.4	7.1	852	12	B1949774	B1949774 HVSME1001
	14	74.4	7.1	854	10	BF261766	BF261766 HV.CEA000
	15	73.4	7.0	676	29	BZ564057	BZ564057 Pacs2-164
C	16	72	6.9	949	29	CNS031R8	AL223901 Tetraodon
	17	72	6.9	1536	13	BQ064626	BQ064626 AGENCOURT
	18	71	6.8	2598	11	AY103647	AY103647 Zea mays
	19	70.8	6.7	779	14	CB642703	CB642703 OSJNEB03A
C	20	70.6	6.7	1170	14	CD496623	CD496623 CDA23-C11
	21	70.4	6.7	616	13	BQ779181	BQ779181 946117E08
	22	70.4	6.7	1204	29	BZ558963	BZ558963 Pacs2-164
	23	70.4	6.7	1491	11	AY104431	AY104431 Zea mays
	24	70.2	6.7	759	14	CB643463	CB643463 OSJNEB04C
	25	70.2	6.7	856	14	CB645086	CB645086 OSJNEB06J
	26	70.2	6.7	877	14	CB620195	CB620195 OSIIEA05D
	27	70.2	6.7	882	14	CB668745	CB668745 OSJNEA16L
	28	69.8	6.6	616	29	CNS03VVH	AL262934 Tetraodon
	29	69.4	6.6	859	14	CB650537	CB650537 OSJNEB15A
	30	69.4	6.6	907	14	CB667927	CB667927 OSJNEA15I
	31	69	6.6	624	13	BQ606324	BQ606324 BRY 2176
	32	69	6.6	935	29	CNS006XX	AL066051 Drosophil
	33	69	6.6	1011	29	BZ563437	BZ563437 Pacs2-164
	34	68.8	6.6	712	13	BU415918	BU415918 603670159
	35	68.6	6.5	753	14	CB647898	CB647898 OSJNEB11A
	36	68.6	6.5	778	14	CB675225	CB675225 OSJNEB10N
	37	68.6	6.5	789	14	CB623003	CB623003 OSIIEA10G
	38	68.6	6.5	789	14	CB623065	CB623065 OSIIEA10I
	39	68.6	6.5	792	14	CB623042	CB623042 OSIIEA10H
	40	68.6	6.5	801	29	BZ532691	BZ532691 OGALJ67TC
	41	68.6	6.5	806	14	CB622999	CB622999 OSIIEA10G
	42	68.6	6.5	812	14	CB625663	CB625663 OSIIEA15B
	43	68.6	6.5	820	14	CB623063	CB623063 OSIIEA10I
	44	68.6	6.5	838	14	CB622964	CB622964 OSIIEA10F
	45	68.6	6.5	839	14	CB669047	CB669047 OSJNEB01E

ALIGNMENTS

RESULT 1
BI651236
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BI651236
603298328F1 NCI_CGAP_Mam3 Mus musculus cdna clone IMAGE:5338806 5',
mRNA sequence.
BI651236
EST.
Mus musculus (house mouse)
Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 688)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LHAM11860 row: h column: 07
High quality sequence stop: 688.


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Db      301  GTATCTGGCATTTCTGGGATTGGCTTATAACACCCGGTACCTATATAGCCGGAATGCCA 360
Qy      557  GCATCCCGCTGAAGGACATCAGCCGACCGACCGCGCGCGCGATGCTGATCCACATCGGCC 616
Db      361  GGATCAGGGTAAAGATATCTCACGGTCTCAGCGTGGGAGAAATGGTAATCCATATTGGGA 420
Qy      617  GCACCAAGACC 627
Db      421  GAAGCGAACC 431

RESULT 3
LOCUS   BI650191                563 bp    mRNA    linear    EST 12-SEP-2001
DEFINITION 603296288F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5336853 5',
mRNA sequence.
ACCESSION BI650191
VERSION   BI650191.1 GI:15564427
KEYWORDS EST.
SOURCE    Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 563)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNL at:
          http://image.llnl.gov
          Plate: LHAM1855 row: f column: 22
          High quality sequence stop: 563.
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              /clone="IMAGE:5336853"
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              /dev_stage="10 months"
              /lab_host="DH10B"
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              /note="Organ: mammary; Vector: pCMV-SPORT6; Site.1: Sali;
              Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
              Library constructed by Life Technologies. Investigators
              providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
              Reference for transgenic model: Xu et al., Nature Genetics
              22, 37-43 (1999)."
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BASE COUNT 143 a 133 c 149 g 138 t
ORIGIN
Query Match 17.3%; Score 181.2; DB 12; Length 563;
Best Local Similarity 76.6%; Pred. No. 7.7e-23;
Matches 222; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy      760  GTGGCCGCCCCAGCGCCAGCGAGCTGAGCACCAGCGGCGCTGGAGGGCATCTTCGAG 819
Db      1  GTTGCGCGCATCTGCCACAGCGAGCTATCACTCGCGCCCTGGAGGGATTTTGAA 60
Qy      820  GCCACCCACCGCTGATCTACGGCCCAAGGACGACGCGCGCTACCTGGCGCTGG 879
Db      61  GCAACTCATCGATTGATTACGGCGCTAAGGATGACTCTGGTCAGAGATACCTGGCGCTGG 120
Qy      880  AGCGGCGCACAGCGCGCGGTGGGCGCGCGCGACATGCGCGCGCGGGGTGAGCATC 939
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Db      121  TCTGGACACAGTCCCGTGTCTGGAGCCGCGGAGATATGCCCGCTGAGTTTCAATA 180
Qy      940  CCGGAGATCATGAGCGCGCGCTGGACCAACGTAACATCTGTATGATGAACATCATCCGC 999
Db      181  CCGGAGATCATGCAAGCTGGTGGCTGGACCAATGTAATATTGTCATGAATATATCCGT 240
Qy      1000  AACCTGACAGCAGACCGCGCGCATGGTGGCGCTGCTGGAGGACGCGGA 1049
Db      241  AACCTGATAGTGAACAGGCGCAATGGTGGCGCTGCTGGAGATGGCGGA 290

RESULT 4
LOCUS   AW212478/c            340 bp    mRNA    linear    EST 03-DEC-1999
DEFINITION u089c09.x1 NCI_CGAP Mam3 Mus musculus cDNA clone IMAGE:2649712 3',
similar to SW:RECR_BPPI P06956 RECOMBINASE CRE. [1] ;, mRNA
sequence.
ACCESSION AW212478
VERSION   AW212478.1 GI:6518565
KEYWORDS EST.
SOURCE    Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 340)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL  Unpublished
COMMENT   Other ESTs: u089c09.Y1
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
          DNA Sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNL at:
          www-bio.llnl.gov/bbrp/image/image.html
          MGI:1030164
          Seq primer: -40UP from Gibco
          High quality sequence stop: 158.
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              /strain="129,C57BL/6J,FVB/N"
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              /clone="IMAGE:2649712"
              /tissue_type="tumor, gross tissue"
              /dev_stage="10 months"
              /lab_host="DH10B"
              /clone_lib="NCI_CGAP_Mam3"
              /note="Organ: mammary; Vector: pCMV-SPORT6; Site.1: Sali;
              Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
              Library constructed by Life Technologies. Investigators
              providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
              Reference for transgenic model: Xu et al., Nature Genetics
              22, 37-43 (1999)."
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BASE COUNT 75 a 100 c 79 g 86 t
ORIGIN
Query Match 15.1%; Score 158.8; DB 9; Length 340;
Best Local Similarity 76.0%; Pred. No. 7.2e-19;
Matches 196; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy      792  CACCGCGCGCTCGAGGGCATCTTCGAGGCCACCCACCGCTGATCTACGCGCGCCAGGA 851
Db      293  CAACTCGCGCTCGAAGGGATTTTGAAGCAACTCATCGATTGATTAGGGCGCTAAGGA 234
Qy      852  CGACAGGGCGCGGTACCTGCGCTGGAGCGGCAAGCGCGCGGTGGCGCGCGCGCGCG 911
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Db	233	TGATTCTGGTCAAGATACCTCTGGGCTTGGTCTGGACACAGTGCCTGGAGCGCGCG	174
Qy	912	CGCATGCGCGCGCGCGCGTGAACATCCCGAGATCATGCAGCGCGCGCTGGACCA	971
Db	173	AGATATGCGCGCGCTGGAGTTTCAATACCGAGATCATGCAAGCTGGTGGTGGACCA	114
Qy	972	CGTGAACATCGTGATGAACTACATCCGCAACCTCTGGAACGCGACCGCGCCATGTGCG	1031
Db	113	TGTAATAATTTGTATGAACATATATCCCTGTAAGTGTGAAACAGGCGCAATGTGCG	54
Qy	1032	CCTGCTGGAGCGCGCA	1049
Db	53	CCTGCTGGAAGATGGCGA	36
RESULT 5	AW211972/c		
LOCUS	AW211972	338 bp	linear
DEFINITION	uo79f01.x1 NCI_CGAP Mam3 Mus musculus cdna clone IMAGE:2648761 3', similar to SW:RECR_BPPI P06956 RECOMBINASE CRE. [1] ;, mRNA		
ACCESSION	AW211972		
VERSION	AW211972		
KEYWORDS	EST.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 338)		
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
JOURNAL	Unpublished		
COMMENT	Other ESTs: uo79f01.v1 Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Lohar Hennighausen Ph.D., Chu-Xia Deng Ph.D. cdna Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html		
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	High quality sequence stop: 151.		
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	/clone_lib="NCI_CGAP Mam3"		
	/note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr. Library constructed by Life Technologies. Investigators providing samples: Lohar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999)."		
BASE COUNT	78 a 93 c 82 g 85 t		
ORIGIN			
	14.3%; Score 150.6; DB 9; Length 338;		
Query Match	Best Local Similarity 76.7%; Pred. No. 2.1e-17;		
Matches	197; Conservative 0; Mismatches 59; Indels 1; Gaps 1;		
Qy	793	ACCGGGCGCTGAGGCGCATCTTCGAGGCGAACCACCGCTGATCTACGCGCGCAAGAC	852

Matches	228;	Conservative	0;	Mismatches	110;	Indels	5;	Gaps	3;
Qy	319	CGCGCAGCGCCTGCCCCCGCCAGCGACACGACGACGCGCTGCTGATCGCGCGC	378						
Db	2	CGTCGTCGGGCTGCCACGACCAAGTGACAGCAATGCTGTTTCACTGGTTATCGCGGG	61						
Qy	379	ATCCGCAAGGAGACGTGGACGCCGCGGAGCGCGCCAAAGCAGGCCCTTGGCCTTCGAGCGC	438						
Db	62	ATCCGAAAAGAAAAAGCTTGATGCGCGGTGAACGTGCAAAACAGGCTCTAGCGTTCGAAACGC	121						
Qy	439	ACCGACTTCGACCAAGGTGCGCAGCGCTGATGGAGAACAGCGACCGCTGCCAGGACATCCGC	498						
Db	122	ACTGATTC-ACCAAGTTCTGTTCTCATGTGAAATAGCGATCGCTGCCAGGATATACGT	180						
Qy	499	AACCTGGCCTTCTCTGGGCA-TCGGCTACAAACACCCTGCTGGCATCGCCAGATCGCGCG	557						
Db	181	AATCTGGCATTTGGGGGATTTGCTTATAACACCCTGTTACGTATAGCCGAAATTGNAG	240						
Qy	558	CATCCGG- ---TGAAGGACATCAGCCGCAACGACGGCGCGCGCATGCTGATCCACATCGG	614						
Db	241	GATCCANGGGTTAAAGATTCTTAGCTTTGACGTGGAGAAAAATGTTTATCCATATGTG	300						
Qy	615	CCGCACCAAGACCTGTGTGACACCGCGCGCGCTGGAGAAGGCC	657						
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RESULT 7	BI556329	836 bp	linear	EST 05-SEP-2001
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DEFINITION	musRNA sequence.			
ACCESSION	BI556329			
VERSION	BI556329.1	GI:15443643		
KEYWORDS	EST.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;			
REFERENCE	1 (bases 1 to 836)			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11734 row: p column: 12 High quality sequence stop: 790. Location/Qualifiers 1..836			
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/notes="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Salt;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
208 a 218 c 224 g 186 t
BASE COUNT
ORIGIN

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Query Match		8.2%; Score 86; DB 12; Length 836;
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Matches 104; Conservative		0; Mismatches 30; Indels 0; Gaps 0;
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Db	160	ATGCCCGAGGCGTTTTCTGAGCATACCGGAGATCATGCAAGCTGCTGGCTGGACCAATGTA 219
QY	976	AACATCGTGATGAATACATCCGCAACTTGGACAGCGAGACCGCGCCATGGTGCGCCCTG 1035
Db	220	AATATTGTCATGAATATATCCCTAACCTGGATAGTAACACAGGGGCAATGGTGCGCCCTG 279
QY	1036	CTGGAGGACGGCGA 1049
Db	280	CTGGAAGATGGCGA 293
RESULT 8		
CC405275/c		
LOCUS	PUHJX22TD	ZM 0.6-1.0 KB Zea mays genomic clone ZMBMTa468C20,
DEFINITION	822 bp	DNA linear GSS 19-MAY-2003
	genomic survey sequence.	
ACCESSION	CC405275	
VERSION	CC405275.1	GI:30885365
KEYWORDS	GSS.	
SOURCE	Zea mays	
ORGANISM	Zea mays	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	
REFERENCE	1	(bases 1 to 822)
AUTHORS	Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick ,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennetzen,J.	
TITLE	Maize Genomics Consortium	
JOURNAL	Unpublished	
COMMENT	Other GSs: PUHJX22TB	
	Contact: Cathy Whitelaw	
	TIGR	
	9712 Medical Center Drive, Rockville, MD 20850, USA	
	Tel: 301-838-5843	
	Fax: 301-838-0208	
	Email: whitelaw@tigr.org	
	Seq primer: TF	
	Class: sheared ends.	
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Matches 270; Conservative 0; Mismatches 256; Indels 12; Gaps 2;		
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Db	680	GGCGCGTGGCTGACAGAGGCCACCGGACGAGG-----AGTACCTGCAGTACGTGTC 627
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Db	626	CCGGAACGCGAGGAGTTTCGGCGGATCGGCTGGTCCGTGCTCGAGTTCTCTCTGGGACA 567
QY	174	CTGGGCGCGCTCGTGAAGCTGAAACACCGCAAGTGGTTCCCGCCGAGCCGAGGACGT 233
Db	566	CAAGTACGCGCGCTGCAAGTGCTCTCTTCCAAGCGCTCTCTGCGCGCGCGCGCGGCA 507

Qy	234	GC	G	A	C	T	A	C	T	A	C	T	G	C	T	-----GT	A	C	T	A	C	G	C	C	G	G	C	C	T	G	G	C	C	T	G	G	C	T	G	G	A	A	G	A	G	A	C	A	T	C	C	A	287
Db	506	GC	A	C	G	C	G	A	C	A	C	G	T	G	A	G	G	C	A	G	T	A	C	C	A	G	G	C	A	G	T	T	C	T	G	T	G	G	C	T	G	C	T	G	C	T	447						
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Db	446	GC	A	A	G	A	A	C	G	G	G	C	A	C	A	T	G	A	A	C	A	T	G	A	A	C	G	G	G	G	T	C	T	G	C	A	C	A	G	A	C	G	A	387									
Qy	348	C	A	G	C	A	A	C	G	C	G	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	407					
Db	386	GT	G	A	A	C	A	A	T	G	C	A	T	G	C	A	T	G	C	A	T	G	C	A	T	G	C	A	T	G	C	A	T	G	C	A	T	G	C	A	T	G	C	A	327								
Qy	408	GC	G	C	G	C	C	A	A	G	C	G	C	C	T	T	C	G	A	G	C	A	C	A	G	A	C	T	T	C	A	C	A	G	G	T	G	C	C	A	G	C	T	G	A	467							
Db	326	C	T	C	G	G	C	G	T	C	G	C	G	C	G	C	T	C	A	G	T	G	C	C	C	G	A	C	G	G	T	G	C	C	C	C	G	G	A	G	A	T	267										
Qy	468	GG	A	A	C	A	G	A	C	C	G	T	G	C	A	G	A	T	C	C	G	A	A	C	T	T	G	G	C	T	T	C	T	G	G	C	A	T	G	C	T	A	C	A	527								
Db	266	GG	T	C	C	G	G	T	T	C	C	A	G	T	C	C	A	G	G	C	G	A	T	A	C	G	T	C	T	G	G	G	A	A	C	C	C	A	G	G	G	C	A	T	207								
Qy	528	C	A	C	C	T	G	C	T	G	C	A	T	G	C	C	C	G	A	T	G	C	C	C	G	C	A	T	C	G	C	T	G	A	A	G	A	C	A	T	C	A	C	C	G	A	C	585					
Db	206	C	T	A	T	G	T	G	A	C	T	A	C	G	C	A	T	C	T	T	C	C	C	A	C	G	C	A	C	T	G	C	A	C	A	C	C	G	C	G	C	T	C	149									

RESULT	9				
BZ728954/c					
LOCUS	BZ728954	838 bp	DNA	linear	GSS 03-MAR-2003
DEFINITION	OGEDN92TM	ZM_0.7_1.5_KB	Zea mays	genomic clone ZMMBMa0251P16,	
				genomic survey sequence.	

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
B2728954	B2728954.1	GI:28702202	GSS.	Zea mays	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	Whiteclaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakev, N.

TITLE
JOURNAL
COMMENT

A.W., RUNDENBERG, J., ROBBINS, D. and LAKEY, N.
Consortium for Maize Genomics
Unpublished
Other GSSs: OGEDN92TC
Contact: Cathy Whitelaw
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org

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Seq primer: TR
Class: sheared ends.
FEATURES
    Location/Qualifiers
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122 a 242 c 307 g 157 t
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Best Local Similarity	46.9%;	Pred. No. 4.2e-05;		
Matches 294;	Conservative	0;	Mismatches 327;	Indels 6;
				Gaps 1;

QY 381 CCGCAAGAGGAACGTGGACGCGCGGAGCGCGCCAGCAGGCCCTGGCCCTTCGAGCGCAC 440

Db	644	CAGCACCAACAACTGGGCCACTTCCAGCTCGTGCTCAGCGCCATCGGCAACTTCTCGAT	585
Qy	441	CGACTTCGACCCAGGTGGCGACGCTGATGAGAAACAGCGACCGCTGCCAGGACATCCGCAA	500
Db	584	CATCTCCATTGCCGTGGGATGGTCACTGAGATCATGTCATGCCGATTGACACCG	525
Qy	501	CTTGGCTTCTTGGGATTCGCTTACAACACCTTGTGCGCATGCCGAGATPGCCCGCAT	560
Db	524	CGGTAACGGGATGGCATCGACACCTTCCTCGTCTCTCATCGCGCGCATCCCATCGC	465
Qy	561	CCG-----CGTGAAGACATCAGCGCACCCGACGGCGCGCATGCTGATCCACATCGG	614
Db	464	CATGCCACCGTGTCTTCCTGTCACCATGGCCATCGGCTCCACCGCTGTCCACGAGG	405
Qy	615	CCGACCAAGACCTGTGTGACACCGCGCGTGGAGAAGCCCTGAGCCTGGCGGTGAC	674
Db	404	CGCCATCACAAAGCGCATCGGCCATCGAGGAGATGGCGGCATGACGTGCTCTCGAG	345
Qy	675	CAAGCTGGTGGAGCGCTGGATCAGCTGTAGGGGGTGGCGACGACCCCAACACTACCT	734
Db	344	CGACAAGCGGCACCCTCAACCTCAACAGCTCACCGTCGACAAAGACCCCTCATCGAGT	285
Qy	735	GTTCTGCGCGTGGCGAAGAACGCGTGGCGGCCCGCCAGCGCCACACGAGCGTGGACAC	794
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Qy	795	CCGGCCCTTGAGGGCATTTTCGAGGCCACCCACCGCTGATCTACGGCGCCCAAGGACGA	854
Db	224	CGAAGACGAGACGCCATCGACACCTGCATCGTCGGCATGCTCGCCGACCCCAAGGAGC	165
Qy	855	CAGCGGCACGGCTACCTGGCCTTGGAGCGGCGCACAGCGCCCGGTGGGCGCGCCCGCA	914
Db	164	CCGGCCGGGATCAAGGAGGTGCATTTCTCCCTTCAACCCGCTTGAGAAGCGCACGGC	105
Qy	915	CATGGCCGCGCGCGCTGAGCATCCCGGAGATCATGACGCGCGCGGTGGACCAACGT	974
Db	104	CATCACCTATCATGACGGCAACGGGACTTGCACAGGCTCAGCAAGGCGCCCGCGAGCA	45
Qy	975	GAACTCGTGATGAACCTACATTCGCAA	1001
Db	44	GATCATCGAGCTGTGCCGATGACAA	18

RESULT 10	
FR0013439	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	

UNCLASSIFIED

REFERENCE	AUTHORS	TITLE
1	Smith, J. D.	Effect of temperature on the rate of reaction of hydrogen peroxide with ferrous sulfate
2	Johnson, R. E.	Investigation of the kinetics of the reaction of hydrogen peroxide with ferrous sulfate in the presence of ceric sulfate
3	Miller, L. A.	Study of the reaction of hydrogen peroxide with ferrous sulfate in the presence of ceric sulfate at various temperatures
4	White, C. H.	Reaction of hydrogen peroxide with ferrous sulfate in the presence of ceric sulfate: a kinetic study
5	Green, P. M.	Kinetics of the reaction of hydrogen peroxide with ferrous sulfate in the presence of ceric sulfate
6	Brown, S. L.	Effect of ceric sulfate on the reaction of hydrogen peroxide with ferrous sulfate
7	Black, T. R.	Reaction of hydrogen peroxide with ferrous sulfate in the presence of ceric sulfate: a kinetic study
8	Gray, W. J.	Reaction of hydrogen peroxide with ferrous sulfate in the presence of ceric sulfate: a kinetic study
9	Hall, K. L.	Reaction of hydrogen peroxide with ferrous sulfate in the presence of ceric sulfate: a kinetic study
10	Young, M. N.	Reaction of hydrogen peroxide with ferrous sulfate in the presence of ceric sulfate: a kinetic study

COMMENT

422

FEATURES

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1. .288
/organism="Takifugu rubripes"
/mol_type="genomic DNA"
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Matches	93	Conservative	0	Mismatches 22	Indels 0
Gaps	0				
Qy	1	ATGCCCAAGAGAGAGAGAGTGTGAGCAACCTGCTGACCGGTGCACCAAGAACCTGCCGCCGCC 60			
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Qy	61	CTGCCCGTGGAGCCACAGCGACGAGTGGCGCAAGAACCTGTATGGACATGTTTCC 115			
Db	114	TTACCGGTGATGATCAACAGTGTATGAGTTCGCCAAGAACCTGTATGGACATGTTTTC 168			
RESULT 11					
CNS0091P/c					
LOCUS	CNS0091P	925 bp	DNA	linear	GSS 03-JUN-1999
DEFINITION	Drosophila melanogaster genome survey sequence TET3 end of BAC #				
	BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.				
ACCESSION	AL053013				
VERSION	AL053013.1	GI:4934461			
KEYWORDS	GSS.				
SOURCE	Drosophila melanogaster (fruit fly)				
ORGANISM	Drosophila melanogaster				
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
REFERENCE	1 (bases 1 to 925)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)				
COMMENT	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm .				
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Matches	52	Conservative	184	Mismatches 134	Indels 0
Gaps	0				
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Db	924	SBSCSCSCSCSB9C8SSSSMTSSNSBSCSCSSBSSSSTSSSSSSSSSSSSSSSS 865			
Qy	612	CG8CCGACCAAGACCTGTTGAGACCGCGCGCGGTGGAGAGCCCTGAGCTGGGCGT 671			

and DNA sequencing were performed in the OD Anderson lab (all other authors)."
BASE COUNT 135 a 274 c 212 g 106 t
ORIGIN

Query Match 7.1%; Score 74.6; DB 13; Length 727;
Best Local Similarity 45.4%; Pred. No. 0.00079;
Matches 269; Conservative 0; Mismatches 324; Indels 0; Gaps 0;
QY 454 GTGCGCAGCTGATGAGAACAGCAGCGCTGCCAGGACATCCGCAACCTGCGCTTCCTG 513
Db 81 GTCTGCTACGGCGTGTGTCGCAACAACTCCCGCGGCAACAGAGTGTGCGAGCTTAC 140
QY 514 GCATCGCTCAACACACCTGCTGCGCATCGCGAGATCGCCGATCGCGGTGAGAC 573
Db 141 AGTCTCAAGGGCTCACCGCATGCGCATCTACTTCGCGGACGCCAAGGCCCTTCCCG 200
QY 574 ATCAGCCGACCGAGCGGCGCGCATGCTGATCCACATCGCGCGGCAACAGACCTGGT 633
Db 201 CTCGCGGCTCGGCATCGGCTCATCTCGAGCTCGCGGACCGAGCTGTCGGCCAGC 260
QY 634 AGCACCAGCGGTGGAAGAGCCCTGAGCCTGAGCGGTGACCAAGCTGGTGGAGCGTGG 693
Db 261 CTCGCGGCAACCGCTCCCAACCGCGCACTGCGGTCCGGGATAAGCTCAGGCCCTACTAT 320
QY 694 ATCAGCGTGGCGGTGCGGACGACCCCACTACCTGTTCTGCGGCTGCGGCAAG 753
Db 321 CCGGGGTGAACATCAAGTATCATCGCGCGGCAACAGAGTCTCTGGGCGGCGACACG 380
QY 754 AACCGCGTGGCGCGCGCGGCGCATGCTGATCCACATCGCGCGGCAACAGACCTGAG 813
Db 381 AACATCGTCCGCGCATACGAACTCAACGCGGCTCGCGGCGCGGCTCGCGCC 440
QY 814 TTCAGGCGCACCGCGCTGATCTACGCGCGCAAGACGACAGCGGCTGACCTG 873
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QY 934 AGCATCCCCAGATCATGCGCGCGCGGCGGTGACCAACGTGACATGCTGATCAATC 993
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RESULT 13
BI949774
LOCUS
DEFINITION
BI949774 852 bp mRNA linear EST 19-OCT-2001
HVSME10015024f Hordeum vulgare spike EST library HVCDNA0012
(Fusarium infected) Hordeum vulgare subsp. vulgare cDNA clone
HVSME10015024f, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BI949774.1 GI:16291326
EST.
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
1. (bases 1 to 852)
Wing, R., Muehlbauer, G.J., Close, T.J., Kleinhofs, A., Wise, R., Heinen
S., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T.,
Simmons, J., Fenton, R.D., Malatrasi, M., Choi, D.W., Oates, R. and Main
D.
Development of a genetically and physically anchored EST resource
for barley genomics: Fusarium infected Morex spike cDNA library
Unpublished
Contact: Wing RA

Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 560
Seq primer: AATTAACTTCACTAAAGGG
High quality sequence stop: 735.
Location/Qualifiers
1. 852
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(Fusarium infected)"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Plants were grown at the University of Minnesota in
the GJ Muehlbauer lab; spikes were harvested and snap
frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium
graminearum inoculation (Heinen). In the TJ Close lab at
the University of California, Riverside, total RNA was
prepared from each sample pool, equal quantities of all
eight RNA pools were combined, poly(A) RNA was purified
from the mixture, one primary unamplified cDNA library was
made, and 1 million pfu were in vivo excised to give
pBluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi
). Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT 163 a 311 c 262 g 113 t 3 others
ORIGIN

Query Match 7.1%; Score 74.4; DB 12; Length 852;
Best Local Similarity 47.4%; Pred. No. 0.00087;
Matches 222; Conservative 0; Mismatches 246; Indels 0; Gaps 0;
QY 579 CCGCAGCGCGCGCGCGCATGCTGATCCACATCGCGCGGACCAAGACCTGTGTGAGCAC 638
Db 57 CCGCAACTCGGCATCGGCTCATCTCGACATCGGCAACGACGCTGCCAACATCGC 116
QY 639 CGCGCGGTGGAGAGCGCTCGAGCTCGCGGTGACCAAGCTGCTGAGCGCTGATCAG 698
Db 117 CGCAGACCTCAACGCGGCTCTCTGGGTCCAGAACAAAGCTGCGGCGCTTACCTGTC 176
QY 699 CGTGGCGGTGGCGCGAGACCCCAACTACTCTGTTCTGCGCGGTGCGCAAGAACCG 758
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QY 759 CGTGGCGGCG 818
Db 237 CCGCGCGCGCATCGCAACTCAACGCGGCGCTCTCGCGGCGGCGCGCGCGCGCGCG 296
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Db 297 GGTGTCACCTCATCCGTTTGAAGAGTGGCCAACTCTTCCCGCGCTCCCGCGCGGT 356

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 Db 417 GCTGGCCAAAGCTTACCCCTACTTTCGGGTACCGTGACAAACCCCGGAGCATGAGCCTGAA 476
 QY 999 CAACCTGGACGAGACCGCGCGCATGTTGGCTCTGCTGGAGACGG 1046
 Db 477 CTACGGACGTTCCAGCGCGGCACACCGCTGCGTGACCAACAACGG 524

RESULT 14

BF261766

LOCUS

DEFINITION

BF261766 854 bp mRNA linear EST 23-OCT-2001
 HV_Cea0002C17f Hordeum vulgare seedling green leaf EST library
 cDNA clone HV_Cea0002C17f, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Hordeum vulgare subsp. vulgare
 Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
 ; Triticeae; Hordeum.

REFERENCE

AUTHORS

1. (bases 1 to 854)
 Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D.,
 Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi
 D.W., Fenton,R.D., Oates,R. and Main,D.

TITLE

Development of a genetically and physically anchored EST resource
 for barley genomics: Blumeria infected incompatible (Mla13)
 seedling leaf cDNA library

JOURNAL

COMMENT

On Nov 17, 2000 this sequence version replaced gi:11192753.
 Contact: Wing RA
 Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu

Total hq bases = 509

Seq primer: AATTACCTCACTAAAGGG

High quality sequence stop: 727.

Location/Qualifiers

1..854

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/mol_type="mRNA"

/cultivar="Cil16155 (Mla13)"

/db_xref="taxon:112509"

/clone="HV_Cea0002C17f"

/tissue_type="seedling green leaf"

/lab_host="TJC121"

/clone_lib="Hordeum vulgare seedling green leaf EST

library HVCDA0004 (Blumeria challenged)"

/notes="vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;

C.I. 16155 (Mla13) plants were greenhouse grown in the R

Wise lab at Iowa State University, Ames, IA; 7 day old

green seedlings were challenged with isolate A27 (AvrMla13

) of Blumeria graminis f. sp. hordei, and leaves were

harvested 20 and 24 hr post-inoculation and snap frozen;

uninoculated leaves were harvested 20 hr post-inoculation

(Wei, Wise). In the TJ Close lab at the University of

California, Riverside, total RNA was prepared from each

sample pool, equal quantities of all three RNA pools were

combined, poly(A) RNA was purified from the mixture, one

cDNA library was made, and 1 million pfu were in vivo

excised to give pBluescript SK(-) cDNA phagemids (Choi,

Close). Phagemids were plated and picked at the Clemson

University Genomics Institute (CUGI) (Begum, Palmer,

Frisch, Atkins and Wing). Plasmid DNA preparations, DNA

sequencing and sequence analysis were performed at CUGI
 (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
 The sequence has been trimmed to remove vector sequence
 and contains a minimum of 100 bases of phred value 20 or
 above. For more details on library preparation and
 sequence analysis see
 http://www.genome.clemson.edu/projects/barley. To order
 this clone see http://www.genome.clemson.edu/orders/Also
 see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT

ORIGIN

151 a 304 c 249 g 149 t 1 others
 Query Match 7.1%; Score 74.4; DB 10; Length 854;
 Best Local Similarity 47.4%; Pred. No. 0.00087;
 Matches 222; Conservative 0; Mismatches 246; Indels 0; Gaps 0;

QY 579 CCGCAGCGAGCGCGCGCATGCTGATCCATCGCGCGGACCAAGACCTGTGTGAGCAC 638
 Db 258 CCGCAACTCCGGCATCGGCTCATCTCCGACATCGGCAACGACGCTCGCAACATCGC 317
 QY 639 CGCGCGCGTGGAGAGGCGCTGAGCGCTGAGCGTGACCAAGCTGTTGGAGCGCTGATCAG 698
 Db 318 CGCAGACCTCCAGCGCGGCTCTTGGGTCCAGAAACAGCTGCGGCGCTTACTACCGCTGC 377
 QY 699 CGTGAGCGCGTGGCGGAGACCCCAACTACTCTTCTGCCGCGTGGCAAGAACGG 758
 Db 378 CGTGAACATCAAGTACATCGCGCGGCAACGAGGTGCATGGCGGCGCCACGAGCAT 437
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 Db 438 CTTGCGGCGCATGCGCAACCTCAACGCGGCGCTCTCGCGGCGGCGGCGGCGGCGGCGGCGG 497
 QY 819 GGCCACCCCGCGCTGATCTAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 878
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 QY 879 GAGCGGCCACAGCGCGCGCGTGGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 938
 Db 558 GTTCAAGAACGCTTACATGACGGAAGTGGCGCGGCTCTTGGGAGGACCGCGCGCGCGCT 617
 QY 939 CCGCGAGATCATGACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 998
 Db 618 GCTGGCCAAAGCTTACCCCTACTTTCGCTACCGTGACAAACCCCGGAGCATGAGCCTGAA 677
 QY 999 CAACCTGGACGAGACCGCGGCGCATGTTGGCGCTTCTGGAGGACGG 1046
 Db 678 CTACGGACGTTCCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 725

RESULT 15

BZ564057

LOCUS

DEFINITION

BZ564057 676 bp DNA linear GSS 17-DEC-2002
 pacs2-164_4528.y2 pacs2-164 Pseudomonas aeruginosa genomic clone
 pacs2-164_4528, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Pseudomonas aeruginosa
 Pseudomonas aeruginosa
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Pseudomonadaceae; Pseudomonas.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
 Burns,J.L., Kaul,R. and Olsen,W.V.
 Whole-Genome-Sequence variation among multiple isolates of
 Pseudomonas aeruginosa library
 J. Bacteriol., (2002) In press
 Contact: Chris K. Raymond
 Genome Center
 University of Washington

Search completed: December 16, 2003, 03:41:48
Job time : 2673 secs